

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:13:17 ; Search time 122 Seconds
(without alignments)
208.189 Million cell updates/sec

Title: US-09-809-060A-2
Perfect score: 36
Sequence: 1 YNTNTYTLLESQNKQKNEQELLELDKWASLWNWP 36

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries.

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

⚡ Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	122	2 Q6WH50_9HIV1	Q6WH50 human immun
2	36	100.0	853	2 Q80161_9HIV1	Q80161 human immun
3	36	100.0	855	1 ENV_HV1A2	P03378 human immun
4	32	88.9	122	2 Q7ZJR9_9HIV1	Q7ZJR9 human immun
5	32	88.9	122	2 Q9EA82_9HIV1	Q9EA82 human immun
6	32	88.9	122	2 Q9LJN5_9HIV1	Q9LJN5 human immun
7	32	88.9	127	2 Q6V8Z2_9HIV1	Q6V8Z2 human immun
8	32	88.9	141	2 Q6V8Y8_9HIV1	Q6V8Y8 human immun
9	32	88.9	144	2 Q7ZC84_9HIV1	Q7ZC84 human immun
10	32	88.9	144	2 Q7ZCE4_9HIV1	Q7ZCE4 human immun
11	32	88.9	845	2 Q6VA57_9HIV1	Q6VA57 human immun
12	32	88.9	852	1 ENV_HV1S3	P19549 human immun
13	32	88.9	852	2 Q9Z761_9HIV1	Q9Z761 human immun
14	32	88.9	852	2 Q73303_9HIV1	Q73303 human immun
15	32	88.9	855	2 Q9E1R7_9HIV1	Q9E1R7 human immun
16	32	88.9	858	2 Q8Q865_9HIV1	Q8Q865 human immun
17	32	88.9	858	2 Q8Q867_9HIV1	Q8Q867 human immun
18	32	88.9	859	2 Q8Q863_9HIV1	Q8Q863 human immun
19	32	88.9	860	2 Q9E1S7_9HIV1	Q9E1S7 human immun
20	32	88.9	864	2 Q9E610_9PLVG	Q9E610 simian-huma
21	32	88.9	871	2 Q5D7P6_9HIV1	Q5D7P6 human immun
22	32	88.9	871	2 Q5D7Q3_9HIV1	Q5D7Q3 human immun
23	29	80.6	122	2 Q9EAA5_9HIV1	Q9EAA5 human immun
24	29	80.6	122	2 Q9YXN9_9HIV1	Q9YXN9 human immun
25	29	80.6	122	2 Q9YXR6_9HIV1	Q9YXR6 human immun
26	29	80.6	138	2 Q5UC10_9HIV1	Q5UC10 human immun
27	29	80.6	144	2 Q7ZC86_9HIV1	Q7ZC86 human immun
28	29	80.6	144	2 Q7ZC94_9HIV1	Q7ZC94 human immun
29	29	80.6	144	2 Q7ZCB0_9HIV1	Q7ZCB0 human immun
30	29	80.6	144	2 Q7ZCB1_9HIV1	Q7ZCB1 human immun
31	29	80.6	144	2 Q7ZCB7_9HIV1	Q7ZCB7 human immun

32 29 80.6 144 2 Q7ZCE3_9HIV1 Q7ZCE3 human immun
33 29 80.6 199 2 Q8JAL6_9HIV1 Q8JAL6 human immun
34 29 80.6 845 2 Q6JEL6_9HIV1 Q6JEL6 human immun
35 29 80.6 849 2 Q6EFV9_9HIV1 Q6EFV9 human immun
36 29 80.6 849 2 Q7ZC12_9HIV1 Q7ZC12 human immun
37 29 80.6 849 2 Q7ZC14_9HIV1 Q7ZC14 human immun
38 29 80.6 850 2 Q6B4P1_9HIV1 Q6B4P1 human immun
39 29 80.6 858 2 Q6BC08_9HIV1 Q6BC08 human immun
40 29 80.6 859 2 Q7Z940_9HIV1 Q7Z940 human immun
41 29 80.6 868 2 Q7ZC11_9HIV1 Q7ZC11 human immun
42 29 80.6 868 2 Q7ZC13_9HIV1 Q7ZC13 human immun
43 27 75.0 42 2 Q69910_9HIV1 Q69910 human immun
44 27 75.0 117 2 Q6WH02_9HIV1 Q6WH02 human immun
45 27 75.0 120 2 Q4VUP4_9HIV1 Q4VUP4 human immun

ALIGNMENTS

RESULT 1
Q6WH50_9HIV1
ID Q6WH50_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q6WH50;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14715797; DOI=10.1128/JCM.42.1.426-430.2004;
RA Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,
RA Couvea M.I.F.S., Guimarães M.A.M., De Oliveira F.E.,
RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;
RT "Prevalence of human immunodeficiency virus drug resistance mutations
RT and subtypes in drug-naïve, infected individuals in the army health
RT service of Rio de Janeiro, Brazil";
RL J. Clin. Microbiol. 42:426-430(2004).
DR EMBL; AY285046; AAQ68109.1; -; Genomic_RNA.
DR SRR; Q6WH50; 1-105.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; P: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14775 MW; 66674BB2877E73FB CRC64;
Query Match 100.0%; Score 36; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.9e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YNTNTYTLLESQNKQKNEQELLELDKWASLWNWP 36
DB 78 YNTNTYTLLESQNKQKNEQELLELDKWASLWNWP 113
RESULT 2
Q80161_9HIV1
ID Q80161_9HIV1 PRELIMINARY; PRT; 853 AA.
AC Q80161;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Envelope polypeptide.
GN Name=env;
OS Human immunodeficiency virus 1.

OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 RN [1]_TaxID=11676;
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92046357; PubMed=16598383;
 RA Cheng-Mayer C., Shioda T., Levy J.A.;
 RT "Host range, replicative, and cytopathic properties of human
 RT immunodeficiency virus type 1 are determined by very few amino acid
 RT changes in tat and gp120.";
 RL J. Virol. 65:6931-6941(1991).
 DR EMBL; L07422; AAA80324.1; -; Genomic_RNA.
 DR HSP; P04578; 1DLB.
 DR SMR; Q80161; 198-488, 529-623.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Envelope protein; Transmembrane.
 SQ SEQUENCE 853 AA; 97056 MW; 2181503CFD1D14789 CRC64;
 Query Match 100.0%; Score 36; DB 2; Length 853;
 Best Local Similarity 100.0%; Pred. No. 1.6e-26;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 36
 DB 635 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 670
 RESULT 3
 ENV_HV1A2 STANDARD; PRT; 855 AA.
 AC P03378;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN Names=ENV;
 OS Human immunodeficiency virus type 1 (isolate ARV2/SP2) (HIV-1).
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 OC NCBI_TaxID=11685;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
 RX MEDLINE=85090453; PubMed=2578227;
 RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
 RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
 RA Levy J.A., Dina D., Luciw P.A.;
 RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
 RT (ARV-2).";
 RL Science 227:484-492(1985).
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
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 DR EMBL; K02007; AAB59882.1; -; Genomic_RNA.
 DR PIR; A03976; VCLJ2A.
 DR HSP; P04578; 1DLB.
 DR SMR; P03378; 199-490, 539-625.
 DR HIV; K02007; ENV\$SF2.
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Capsid protein; Glycoprotein; Polypeptide; Signal;

KW Structural protein; Transmembrane.
 FT SIGNAL 1 29 Exterior membrane glycoprotein.
 FT CHAIN 30 509 Transmembrane glycoprotein.
 FT CHAIN 510 855
 FT CARBOHYD 87 87 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 129 129 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 140 140 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 154 154 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 158 158 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 190 190 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 200 200 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 233 233 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 244 244 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 265 265 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 279 279 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 298 298 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 304 304 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 341 341 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 358 358 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 364 364 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 388 388 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 394 394 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 400 400 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 408 408 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 445 445 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 461 461 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 610 610 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 615 615 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 624 624 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 636 636 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 815 815 N-linked (GlcNAc...) (Potential).
 FT DISULFID 53 73 By similarity.
 FT DISULFID 118 208 By similarity.
 FT DISULFID 125 199 By similarity.
 FT DISULFID 130 155 By similarity.
 FT DISULFID 221 250 By similarity.
 FT DISULFID 231 242 By similarity.
 FT DISULFID 299 333 By similarity.
 FT DISULFID 380 442 By similarity.
 FT DISULFID 387 415 By similarity.
 SQ SEQUENCE 855 AA; 97438 MW; A38C20573AAC41A2 CRC64;
 Query Match 100.0%; Score 36; DB 1; Length 855;
 Best Local Similarity 100.0%; Pred. No. 1.6e-26;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 36
 DB 637 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 672
 RESULT 4
 Q7ZJR9 9HIV1 PRELIMINARY; PRT; 122 AA.
 ID Q7ZJR9 9HIV1 PRELIMINARY;
 AC Q7ZJR9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 OC NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22800244; PubMed=12921095; DOI=10.1089/08892203223221003;
 RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
 RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M

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RT (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
RT integrase, and env gp41.
RL AIDS Res. Hum. Retroviruses 19:625-629 (2003).
DR ENBL; AY214090; AAO61810.1; -; Genomic_RNA.
DR HSP; P04624; 1JAU.
DR SMR; Q72UR9; 1-105.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Envelope protein.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14745 MW; 2244648573D7BFF9 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLESQOQKNEQELLELDKWSLWNWF 36
DB 82 IYTLLESQOQKNEQELLELDKWSLWNWF 113

RESULT 5
Q9EA82_9HIV1
ID Q9EA82_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q9EA82;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BX922;
RX MEDLINE=20134570; PubMed=106693328; DOI=10.1086/315253;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475 (2000).
DR ENBL; AF190970; AG02332.1; -; Genomic_DNA.
DR HSP; P31872; 1IB0.
DR SMR; Q9EA82; 1-105.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Envelope protein.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14804 MW; CF6AF2DC9EDA9C69 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLESQOQKNEQELLELDKWSLWNWF 36
DB 82 IYTLLESQOQKNEQELLELDKWSLWNWF 113

RESULT 6
Q9IUN5_9HIV1
ID Q9IUN5_9HIV1 PRELIMINARY; PRT; 122 AA.

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AC Q9IUN5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AR36;
RX MEDLINE=20346416; PubMed=10890362; DOI=10.1089/08922220050058425;
RA Masciotra S., Livellara B., Bellosio W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR ENBL; AF226697; AAF76816.1; -; Genomic_DNA.
DR HSP; P12488; 1IM7.
DR SMR; Q9IUN5; 1-105.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Envelope protein.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14779 MW; C9B2C8944C48C614 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLESQOQKNEQELLELDKWSLWNWF 36
DB 82 IYTLLESQOQKNEQELLELDKWSLWNWF 113

RESULT 7
Q6V8Z2_9HIV1
ID Q6V8Z2_9HIV1 PRELIMINARY; PRT; 127 AA.
AC Q6V8Z2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yilmaz G., Midilli K., Turkoglu S., Kuskucu A.M., Bayraktaroglu Z.,
RA Aksozek A., Ozkan E., Calangu S., Altas K.;
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR ENBL; AY347737; AAQ63672.1; -; Genomic_DNA.
DR SMR; Q6V8Z2; 1-107.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Envelope protein.
FT NON_TER 1
FT NON_TER 127
FT NON_TER 127
SQ SEQUENCE 127 AA; 15450 MW; F775D7E19BF78A5B CRC64;

Query Match 88.9%; Score 32; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.4e-23;

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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 IYTLLEESQKQKNEQELLELDKQASLWNWF 36
Db 84 IYTLLEESQKQKNEQELLELDKQASLWNWF 115

RESULT 8
Q6V8Y8_9HIV1
ID Q6V8Y8_9HIV1 PRELIMINARY; PRT; 141 AA.
AC Q6V8Y8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Yilmaz G., Midilli K., Turkoglu S., Kuskucu A.M., Bayraktaroglu Z.,
RA Aksozek A., Ozkan E., Calangu S., Altas K.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347741; AAQ63676.1; -; Genomic_DNA.
DR SMR; Q6V8Y8; 3-82.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 16814 MW; B6A0F119928C26A1 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.6e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 IYTLLEESQKQKNEQELLELDKQASLWNWF 36
Db 98 IYTLLEESQKQKNEQELLELDKQASLWNWF 129

RESULT 9
Q7ZC84_9HIV1
ID Q7ZC84_9HIV1 PRELIMINARY; PRT; 144 AA.
AC Q7ZC84;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with subtype B and non-B HIV-1 strains.";
RL J. Acquir. Immune Defic. Syndr. 33:134-139(2003).
DR EMBL; AY18436; AAO65711.1; -; Genomic_RNA.
DR HSSP; Q89797; 1F23.
DR SMR; Q7ZC84; 11-98.
DR GO; GO:0016021; C:integral to membrane; IEA.
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DR GO; GO:0019031; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 16863 MW; AD6C57B998454949 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 IYTLLEESQKQKNEQELLELDKQASLWNWF 36
Db 113 IYTLLEESQKQKNEQELLELDKQASLWNWF 144

RESULT 10
Q7ZC84_9HIV1
ID Q7ZC84_9HIV1 PRELIMINARY; PRT; 144 AA.
AC Q7ZC84;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22679027; PubMed=12794544;
RX DOI=10.1097/00126334-200306010-00003;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with subtype B and non-B HIV-1 strains.";
RL J. Acquir. Immune Defic. Syndr. 33:134-139(2003).
DR EMBL; AY185376; AAO65651.1; -; Genomic_RNA.
DR HSSP; P12488; 11W7.
DR SMR; Q7ZC84; 11-97.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 16856 MW; 204A5328B6EE248C CRC64;

Query Match 88.9%; Score 32; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 IYTLLEESQKQKNEQELLELDKQASLWNWF 36
Db 113 IYTLLEESQKQKNEQELLELDKQASLWNWF 144

RESULT 11
Q6YA57_9HIV1
ID Q6YA57_9HIV1 PRELIMINARY; PRT; 845 AA.
AC Q6YA57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
```


OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OX Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CM237;
RX MEDLINE=22866095; PubMed=14506784; DOI=10.1089/0892220322280937;
RA Swanson P., Devare S.G., Hackett J. Jr.;
RT "Full-length sequence analysis of HIV-1 isolate CM237: a CRF01_AE/B
inter-subtype recombinant from Thailand.";
RL AIDS Res. Hum. Retroviruses 19:707-712(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CM237;
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY167123; AAC40783.1; -; Genomic_RNA.
DR HSSP; P04578; 1K33.
DR SMR; O6YA57; 1-130, 100-348, 140-480, 529-615.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 845 AA; 95647 MW; 7A6654344CFD02AB CRC64;

Query Match 88.9%; Score 32; DB 2; Length 845;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLEESQKQKNEQELLELDKWSLWNWF 36
|||||
DB 631 IYTLLEESQKQKNEQELLELDKWSLWNWF 662

RESULT 12
ID ENV_HV1S3 STANDARD; PRT; 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN Name=ENV;
OS Human immunodeficiency virus type 1 (isolate SF33) (HIV-1).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11690;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range, replication,
RT and cytopathicity are linked to the envelope region of the viral
RT genome.";
RL J. Virol. 64:4016-4020(1990).
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AY352275; AAC17031.1; -; Genomic_DNA.
DR PDB; 1MEQ; NMR; A=484-506.
DR SMR; P19549; 536-622.
DR HIV; M38427; ENV\$SF33.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW 3D-structure; AIDS; Capsid protein; Glycoprotein; Polypeptide; Signal;
KW Structural protein; Transmembrane.
FT SIGNAL 1 31
FT CHAIN 32 506
FT CHAIN 507 852
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 142 142
FT CARBOHYD 155 155
FT CARBOHYD 159 159
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FT DISULFID 53 73
FT DISULFID 118 206
FT DISULFID 125 197
FT DISULFID 130 156
FT DISULFID 219 248
FT DISULFID 229 240
FT DISULFID 297 331
FT DISULFID 377 439
FT DISULFID 384 412
SQ SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C910D CRC64;

Query Match 88.9%; Score 32; DB 1; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLEESQKQKNEQELLELDKWSLWNWF 36
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DB 638 IYTLLEESQKQKNEQELLELDKWSLWNWF 669

RESULT 13
ID 092761_9HIV1 PRELIMINARY; PRT; 852 AA.
AC 092761;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98178716; PubMed=9519894;
RA McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,

RA Shepard W.H.;
RT "Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in San Francisco Men's Health Study Participants.";
RL AIDS Res. Hum. Retroviruses 14:329-337(1998).
DR EMBL; A025750; AAC40588.1; -; Genomic_DNA.
DR HSSP; P20871; 1CE4.
DR SMR; 092761; 536-622.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 852 AA; 96544 MW; 3C7780DB0611E617 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLEESQOQKNEQELLELDKWASLWNWF 36
Db 638 IYTLLEESQOQKNEQELLELDKWASLWNWF 669

RESULT 14
Q73303_9HIV1
ID Q73303_9HIV1 PRELIMINARY; PRT; 852 AA.
AC Q73303;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96263682; PubMed=8924250;
RA Douglas N.W., Knight A.I., Hayhurst A., Barrett W.Y., Kevany M.J., Daniels R.S.;
RT "An efficient method for the rescue and analysis of functional HIV-1 env genes: evidence for recombination in the vicinity of the tat/rev splice site.";
RL AIDS 10:139-46(1996).
DR EMBL; U36877; AAC5537.1; -; Genomic_DNA.
DR PIR; A53591; A53591.
DR HSSP; P04578; 1DLB.
DR SMR; Q73303; 81-125, 197-488, 536-622.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 852 AA; 96808 MW; A24BA64A133D149B CRC64;

Query Match 88.9%; Score 32; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLEESQOQKNEQELLELDKWASLWNWF 36
Db 638 IYTLLEESQOQKNEQELLELDKWASLWNWF 669

RESULT 15
Q9EIR7_9HIV1

ID Q9EIR7_9HIV1 PRELIMINARY; PRT; 855 AA.
AC Q9EIR7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20442410; PubMed=10984542; DOI=10.1073/pnas.97.19.10532;
RA Cleghorn F.R., Jack N., Carr J.K., Edwards J., Mahabir B., Sill A., McDonald C.B., Connolly S.M., Goodman D., Bennetts R.Q., O'Brien T.R., Weinhold K.J., Bartholomew C., Blattner W.A., Greenberg M.L.;
RT "A distinctive clade B HIV type 1 is heterosexually transmitted in Trinidad and Tobago.";
RT Proc. Natl. Acad. Sci. U.S.A. 97:10532-10537(2000).
RL EMBL; AF277071; AG22514.1; -; Genomic_DNA.
DR HSSP; P31872; 1LBO.
DR SMR; Q9EIR7; 539-625.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 855 AA; 97102 MW; 26271D6CCCCCFFAC CRC64;

Query Match 88.9%; Score 32; DB 2; Length 855;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLEESQOQKNEQELLELDKWASLWNWF 36
Db 641 IYTLLEESQOQKNEQELLELDKWASLWNWF 672

Search completed: March 6, 2006, 16:25:16
Job time : 123 secs

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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:25:38 ; Search time 28.6667 Seconds
(without alignments)
103.825 Million cell updates/sec

Title: US-09-809-060A-2

Perfect score: 36

Sequence: 1 YNTIYTLLESQKQKNEQELLELDKWLNNWF 36

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	36	2	US-08-486-099-3
2	36	100.0	36	2	US-08-484-223B-3
3	36	100.0	36	2	US-08-319-597-3
4	36	100.0	36	2	US-08-475-668A-3
5	36	100.0	36	2	US-08-485-551A-3
6	36	100.0	36	2	US-08-471-913A-3
7	36	100.0	36	2	US-08-485-264A-3
8	36	100.0	36	2	US-09-082-279B-1357
9	36	100.0	36	2	US-08-474-349A-3
10	36	100.0	36	2	US-09-315-304B-1357
11	36	100.0	36	2	US-08-255-208A-3
12	36	100.0	36	2	US-08-973-952-3
13	36	100.0	36	2	US-08-470-896-3
14	36	100.0	36	2	US-08-485-546A-3
15	36	100.0	36	2	US-09-834-784-1357
16	36	100.0	36	2	US-09-515-965A-1357
17	36	100.0	36	2	US-09-350-641C-1357
18	36	100.0	36	2	US-09-350-841A-1357
19	36	100.0	36	2	US-08-487-266A-3
20	36	100.0	36	2	US-09-823-548A-1421
21	36	100.0	36	2	US-10-252-136-3
22	36	100.0	36	2	US-09-657-276-1421
23	36	100.0	36	2	US-08-484-741-3
24	36	100.0	138	2	US-09-570-921-16
25	36	100.0	145	1	US-08-394-021-11
26	36	100.0	145	2	US-09-131-551-11
27	36	100.0	145	2	US-10-000-321-11

Query Match 100.0%; Score 36; DB 2; Length 36;

28 36 100.0 269 2 US-08-965-056-30 Sequence 30, Appl
29 36 100.0 269 2 US-08-965-056-31 Sequence 31, Appl
30 36 100.0 269 2 US-09-257-490-12 Sequence 12, Appl
31 36 100.0 855 2 US-07-956-483-15 Sequence 15, Appl
32 36 100.0 887 2 US-08-472-240A-6 Sequence 6, Appl
33 32 88.9 36 2 US-09-082-279B-856 Sequence 856, App
34 32 88.9 36 2 US-09-315-304B-856 Sequence 856, App
35 32 88.9 36 2 US-09-834-784-856 Sequence 856, App
36 32 88.9 36 2 US-09-515-965A-856 Sequence 856, App
37 32 88.9 36 2 US-09-350-641C-856 Sequence 856, App
38 32 88.9 36 2 US-09-350-841A-856 Sequence 856, App
39 32 88.9 138 2 US-09-570-921-19 Sequence 19, Appl
40 32 88.9 269 2 US-08-965-056-28 Sequence 28, Appl
41 29 80.6 36 1 US-08-073-028-3 Sequence 3, Appl
42 29 80.6 36 2 US-08-360-107A-3 Sequence 3, Appl
43 29 80.6 36 2 US-08-554-616-3 Sequence 3, Appl
44 29 80.6 36 2 US-09-082-279B-1051 Sequence 1051, Ap
45 29 80.6 36 2 US-09-315-304B-1051 Sequence 1051, Ap

ALIGNMENTS

RESULT 1

US-08-486-099-3
; Sequence 3, Application US/08486099
; Patent No. 6013263

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

; NUMBER OF INVENTIONS: B VIRUS TRANSMISSION

; NUMBER OF SEQUENCES: 209

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,099

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-031

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-486-099-3

Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 2

US-08-484-223B-3
; Sequence 3, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

US-08-484-223B-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 3

US-08-919-597-3
; Sequence 3, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

US-08-919-597-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 4

US-08-475-668A-3
; Sequence 3, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

US-08-475-668A-3

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQKEQELLELDKWASLWNWF 36
DB 1 YNTIYTLLEESQNOQKEQELLELDKWASLWNWF 36

RESULT 5
US-08-485-551A-3
Sequence 3, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-3
Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQKEQELLELDKWASLWNWF 36
DB 1 YNTIYTLLEESQNOQKEQELLELDKWASLWNWF 36

RESULT 6
US-08-471-913A-3
Sequence 3, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNITVLLSESONQKNEQELLELDKWASLWNWF 36
Db 1 YNTNITVLLSESONQKNEQELLELDKWASLWNWF 36

RESULT 7

US-08-485-264A-3
; Sequence 3, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-485-264A-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNITVLLSESONQKNEQELLELDKWASLWNWF 36
Db 1 YNTNITVLLSESONQKNEQELLELDKWASLWNWF 36

RESULT 8

US-09-082-279B-1357
; Sequence 1357, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anyer, Mohmed
; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1357
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-1357

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNITVLLSESONQKNEQELLELDKWASLWNWF 36
Db 1 YNTNITVLLSESONQKNEQELLELDKWASLWNWF 36

RESULT 9

US-08-474-349A-3
; Sequence 3, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27; Mismatches 0; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKNEQELLELDKWASLWNWF 36
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DB 1 YNTIYTLLEESQKNEQELLELDKWASLWNWF 36

RESULT 10
US-09-315-304B-1357
; Sequence 1357, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1357
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1357

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27; Mismatches 0; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKNEQELLELDKWASLWNWF 36
|||||
DB 1 YNTIYTLLEESQKNEQELLELDKWASLWNWF 36

RESULT 11
US-08-255-208A-3
; Sequence 3, Application US/08255208A
; Patent No. 6440656
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway Jr., Stephen R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,208A

FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-255-208A-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27; Mismatches 0; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKNEQELLELDKWASLWNWF 36
|||||
DB 1 YNTIYTLLEESQKNEQELLELDKWASLWNWF 36

RESULT 12
US-08-973-952-3
; Sequence 3, Application US/08973952A
; Patent No. 6475491
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/08/973,952A
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 08/481,957
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-08-973-952-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27; Mismatches 0; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKNEQELLELDKWASLWNWF 36
|||||
DB 1 YNTIYTLLEESQKNEQELLELDKWASLWNWF 36

RESULT 13
US-08-470-896-3
; Sequence 3, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION

```
/ NUMBER OF SEQUENCES: 273
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/470,896
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-020
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-08-470-896-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 14
US-08-485-546A-3
/ Sequence 3, Application US/08485546A
/ Patent No. 6518013
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ ADDRESSEE: Matthews, Thomas J.
/ APPLICANT: Wild, Carl T.
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ APPLICANT: Langlois, Alphonse J.
/ TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
/ TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
/ TITLE OF INVENTION: TRANSMISSION
/ NUMBER OF SEQUENCES: 214
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,546A
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/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-028
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-08-485-546A-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 15
US-09-834-784-1357
/ Sequence 1357, Application US/09834784
/ Patent No. 6562787
/ GENERAL INFORMATION:
/ APPLICANT: Barney, Shawn
/ APPLICANT: Guthrie, Kelly
/ APPLICANT: Merutka, Gene
/ APPLICANT: Anwer, Mohmed
/ APPLICANT: Lambert, Dennis
/ TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
/ TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
/ FILE REFERENCE: 7872-043
/ CURRENT APPLICATION NUMBER: US/09/834,784
/ CURRENT FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 09/082,279
/ PRIOR FILING DATE: 1998-05-20
/ NUMBER OF SEQ ID NOS: 1515
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1357
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Core polypeptide
/ US-09-834-784-1357

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36

Search completed: March 6, 2006, 16:27:50
Job time : 28.6667 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:19:28 ; Search time 19 Seconds
(without alignments)
182.305 Million cell updates/sec

Title: US-09-809-060A-2

Perfect score: 36

Sequence: 1 YNTYITLLEESQNOQKNEQLLELDKWASLWNWF 36

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	855	1 VCLJJA2	env polyprotein pr
2	27	75.0	357	2 S21994	envelope protein g
3	27	75.0	357	2 S21996	envelope protein g
4	27	75.0	443	2 C41621	env polyprotein P
5	27	75.0	847	2 T09448	envelope glycoprot
6	27	75.0	847	2 S13289	env protein - huma
7	27	75.0	851	2 S33985	env polyprotein -
8	27	75.0	854	2 S13288	env protein - huma
9	27	75.0	856	1 VCLJ3W	env polyprotein pr
10	27	75.0	856	1 VCLJH3	env polyprotein pr
11	27	75.0	861	1 VCLJSC	env polyprotein pr
12	27	75.0	861	1 VCLJLV	env polyprotein pr
13	25	69.4	358	2 S21998	envelope protein g
14	22	61.1	357	2 S21992	envelope protein g
15	22	61.1	853	2 S54384	envelope polyprot
16	22	61.1	855	1 VCLJZR	env polyprotein pr
17	22	61.1	859	1 VCLJMN	env polyprotein pr
18	21	58.3	856	1 VCLJVL	env polyprotein pr
19	16	44.4	852	2 T12016	envelope glycoprot
20	15	41.7	357	2 S22004	envelope protein g
21	15	41.7	357	2 S22006	envelope protein g
22	15	41.7	357	2 S22006	envelope protein g
23	15	41.7	852	1 VCLJBR	env polyprotein pr
24	15	41.7	859	2 T01672	env polyprotein -
25	13	36.1	357	2 S21990	envelope polyprot
26	13	36.1	843	1 H44001	envelope protein g
27	12	33.3	358	2 S70417	envelope protein g
28	12	33.3	358	2 S22000	envelope protein g
29	12	33.3	358	2 S22002	envelope protein g

RESULT 1

VCLJJA2
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03976
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Shi
Science 227, 484-492, 1985
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A:Reference number: A04003; MUID:85090453; PMID:2578227
A:Accession: A03976
A:Molecule type: DNA
A:Residues: 1-855 <S>
A:Cross-references: UNIPROT:P03378; UNIPARC:UPI000012A00F; GB:K02007; NID:G328658; PIDN:1
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458/
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 36; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 8.3e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESQNOQKNEQLLELDKWASLWNWF 36
Db 637 YNTYITLLEESQNOQKNEQLLELDKWASLWNWF 672

RESULT 2

S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determin
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <ST>
A:Cross-references: UNIPROT:Q78118; UNIPARC:UPI0000178606; EMBL:X61355; NID:G60179; PIDN:
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; UID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>
A:Cross-references: UNIPARC:UPI00000F05F; EMBL:X61355; NID:g60179
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.0%; Score 27; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.8e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWSLWNWF 36
DB 148 EESQNOEKNEQELLELDKWSLWNWF 174

RESULT 3
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; UID:92144209; PMID:1736940
A:Accession: S70422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: UNIPROT:Q78119; UNIPARC:UPI0000104EC6; EMBL:X61356; NID:g60181; PIDN: S21996
A:Experimental source: patient 27L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.0%; Score 27; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.8e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWSLWNWF 36
DB 148 EESQNOEKNEQELLELDKWSLWNWF 174

RESULT 4
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: C41621
R:Butcher, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; UID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443

A:Cross-references: UNIPROT:Q80023; UNIPARC:UPI0000104256; GB:M77230; NID:g328631; PIDN: C41621
A:Note: This virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:424-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 75.0%; Score 27; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 3.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWSLWNWF 36
DB 387 EESQNOEKNEQELLELDKWSLWNWF 413

RESULT 5
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09448
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI000010C516; EMBL:U63632; NID:g1465777; PID: T09448
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.0%; Score 27; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWSLWNWF 36
DB 638 EESQNOEKNEQELLELDKWSLWNWF 664

RESULT 6
S13289
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13289
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Digne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c
A:Reference number: S13288; UID:91043044; PMID:2172833
A:Accession: S13289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-847 <OBR>
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI000017861B
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.0%; Score 27; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWSLWNWF 36
DB 638 EESQNOEKNEQELLELDKWSLWNWF 664

RESULT 7
S33985
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S33985
R:Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:Z11530; NID:G60192; PIDN
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.0%; Score 27; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEQELLELDKWSLWNNF 36
Db 642 EESONQOEKNEQELLELDKWSLWNNF 668

RESULT 8
S13288
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C:Accession: S13288
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13288
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OBR>
A:Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:Q90178; UNIPROT:Q78243; UNIP

Query Match 75.0%; Score 27; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEQELLELDKWSLWNNF 36
Db 645 EESONQOEKNEQELLELDKWSLWNNF 671

RESULT 9
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: A24774
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the en
A:Reference number: A24774; MUID:86218077; PMID:2423250
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: UNIPROT:P31872; UNIPARC:UPI000012A024; GB:K03455; GB:M38432; NID:glu
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 75.0%; Score 27; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEQELLELDKWSLWNNF 36
Db 647 EESONQOEKNEQELLELDKWSLWNNF 673

RESULT 10
VCLJTV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1

VCLJTH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.P.; Dorar
nberger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K020
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,155,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406;
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 75.0%; Score 27; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 6.4e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEQELLELDKWSLWNNF 36
Db 647 EESONQOEKNEQELLELDKWSLWNNF 673

RESULT 11
VCLJSC
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: B28922
R:Guo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
Virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>
A:Cross-references: UNIPARC:UPI0000174A39
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protei
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-861/Product: env polyprotein #status predicted <EPP>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396,
Query Match 75.0%; Score 27; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 6.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEQELLELDKWSLWNNF 36
Db 652 EESONQOEKNEQELLELDKWSLWNNF 678

RESULT 12
VCLJTV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1

A;Title: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03975
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:8509333; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <WAI>
A;Cross-references: UNIPROT:P03377; UNIPARC:UPI000012A013; GB:X02013; NID:g326417; PIDN:
C;Genetics:
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F;517-861/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 75.0%; Score 27; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 6.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 ERSQOQEKNEQELLELDKWASLWNWF 36
DB 652 ERSQOQEKNEQELLELDKWASLWNWF 678
RESULT 13
S21998
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 28
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S21998; S70425
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A;Reference number: S21990
A;Accession: S21998
A;Molecule type: DNA
A;Residues: 1-358 <STEL>
A;Cross-references: UNIPROT:Q78120; UNIPARC:UPI0000178607; EMBL:X61359; NID:g60182; PIDN:
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal
A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70425
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-222,'X',224-358 <STE2>
A;Cross-references: UNIPARC:UPI00000FE72C; EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PIDN:
C;Superfamily: type E retrovirus env polyprotein
Query Match 69.4%; Score 25; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 SQOQEKNEQELLELDKWASLWNWF 36
DB 151 SQOQEKNEQELLELDKWASLWNWF 175
RESULT 14
S21992
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S70424; S21992
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal
A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <ST2>
A;Cross-references: UNIPROT:Q78112; UNIPARC:UPI0000107A48; EMBL:X61358; NID:g60177; PIDN:
A;Experimental source: patient 22
A;Note: submitted to the EMBL Data Library, July 1991
C;Superfamily: type E retrovirus env polyprotein
Query Match 61.1%; Score 22; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 SQOQEKNEQELLELDKWASLW 33
DB 150 SQOQEKNEQELLELDKWASLW 171
RESULT 15
S54384
envelope polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54384
R;Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A;Reference number: S54377
A;Accession: S54384
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-853 <THE>
A;Cross-references: UNIPROT:P12487; UNIPARC:UPI000012A027; EMBL:M22639; NID:g329377; PIDN:
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: polyprotein
Query Match 61.1%; Score 22; DB 2; Length 853;
Best Local Similarity 100.0%; Pred. No. 5.5e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 QOQEKNEQELLELDKWASLWNWF 36
DB 649 QOQEKNEQELLELDKWASLWNWF 670
Search completed: March 6, 2006, 16:26:19
Job time : 20 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	36	100.0	36	3	US-09-809-060-2	Sequence 2, Appli
2	36	100.0	36	4	US-10-252-136-3	Sequence 3, Appli
3	36	100.0	36	4	US-10-351-641-1357	Sequence 1357, Ap
4	36	100.0	36	4	US-10-267-682-3	Sequence 3, Appli
5	36	100.0	36	4	US-10-267-748-3	Sequence 3, Appli
6	36	100.0	36	4	US-10-663-589-38	Sequence 38, Appl
7	36	100.0	36	4	US-10-671-282-38	Sequence 38, Appl
8	36	100.0	36	5	US-10-168-293-3	Sequence 3, Appli
9	36	100.0	36	5	US-10-950-010-3	Sequence 3, Appli
10	36	100.0	36	6	US-11-066-697-1421	Sequence 1421, Ap
11	36	100.0	145	3	US-09-131-551-11	Sequence 11, Appl
12	36	100.0	145	4	US-10-000-321-11	Sequence 11, Appl
13	36	100.0	269	3	US-09-854-816-30	Sequence 30, Appl
14	36	100.0	269	3	US-09-854-816-31	Sequence 31, Appl
15	32	88.9	36	4	US-10-351-641-856	Sequence 856, App
16	32	88.9	70	6	US-11-018-102-13	Sequence 13, Appl
17	32	88.9	269	3	US-09-854-816-28	Sequence 28, Appl
18	32	88.9	285	6	US-11-018-102-11	Sequence 11, Appl
19	29	80.6	36	4	US-10-351-641-1051	Sequence 1051, Ap
20	29	80.6	36	5	US-10-950-010-541	Sequence 541, App
21	27	75.0	27	4	US-10-005-305-58	Sequence 58, Appl
22	27	75.0	27	4	US-10-005-305-73	Sequence 73, Appl
23	27	75.0	27	5	US-10-950-010-125	Sequence 125, App
24	27	75.0	28	4	US-10-005-305-59	Sequence 59, Appl
25	27	75.0	28	4	US-10-005-305-72	Sequence 72, Appl
26	27	75.0	28	5	US-10-950-010-124	Sequence 124, App
27	27	75.0	29	4	US-10-351-641-635	Sequence 635, App

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; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-3

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTNTIYTLLESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTNTIYTLLESQKQKNEQELLELDKWASLWNWF 36

RESULT 3
US-10-351-641-1357
; Sequence 1357, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 1357
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1357

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTNTIYTLLESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTNTIYTLLESQKQKNEQELLELDKWASLWNWF 36

RESULT 4
US-10-267-682-3
; Sequence 3, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas

; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-3

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTNTIYTLLESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTNTIYTLLESQKQKNEQELLELDKWASLWNWF 36

RESULT 5
US-10-267-748-3
; Sequence 3, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
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; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-267-748-3

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36
DB 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 6
US-10-663-589-38
; Sequence 38, Application US/10663589
; Publication No. US20040063637A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-38

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36
DB 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 7
US-10-671-282-38
; Sequence 38, Application US/10671282
; Publication No. US20040122214A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
; TITLE OF INVENTION: their use in therapy
; FILE REFERENCE: TRM-004
```

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; CURRENT APPLICATION NUMBER: US/10/671,282
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/414,439
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-671-282-38

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36
DB 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 8
US-10-168-295-3
; Sequence 3, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Baroudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-3

Query Match 100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36
DB 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 9
US-10-950-010-3
; Sequence 3, Application US/10950010
; Publication No. US20050070475A1
; GENERAL INFORMATION:
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: DUFRESNE, Robert S.
; APPLICANT: BOUDJELLAB, Nissab
; APPLICANT: ROBITAILLE, Martin
; APPLICANT: MILNER, Peter G.
; TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL
; TITLE OF INVENTION: INFECTION
; FILE REFERENCE: 500862001501/REDC-1512
; CURRENT APPLICATION NUMBER: US/10/950,010
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: US 09/623,533
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13651
; PRIOR FILING DATE: 2000-05-17
```

;; PRIOR APPLICATION NUMBER: US 60/134,406
;; PRIOR FILING DATE: 1999-05-17
;; PRIOR APPLICATION NUMBER: US 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; NUMBER OF SEQ ID NOS: 545
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3
;; LENGTH: 36
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
;; OTHER INFORMATION: peptide
US-10-950-010-3

Query Match 100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQKQKNEQELLELDKQWASLNNWF 36
|||||
Db 1 YNTYITLLEESNQKQKNEQELLELDKQWASLNNWF 36

RESULT 10

US-11-066-697-1421
;; Sequence 1421, Application US/11066697
;; Publication No. US20050187159A1
;; GENERAL INFORMATION:
;; APPLICANT: Bridon, Dominique P.
;; APPLICANT: Ezrin, Alan M.
;; APPLICANT: Milner, Peter G.
;; APPLICANT: Holmes, Darren L.
;; APPLICANT: Thibaudau, Karen
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;; TITLE OF INVENTION: COMPONENTS
;; FILE REFERENCE: 500862002301
;; CURRENT APPLICATION NUMBER: US/11/066,697
;; CURRENT FILING DATE: 2005-02-25
;; PRIOR FILING DATE: 2005-09-27
;; PRIOR FILING DATE: 2000-09-07
;; PRIOR APPLICATION NUMBER: 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-15
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1421
;; LENGTH: 36
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-11-066-697-1421

Query Match 100.0%; Score 36; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQKQKNEQELLELDKQWASLNNWF 36
|||||
Db 1 YNTYITLLEESNQKQKNEQELLELDKQWASLNNWF 36

RESULT 11

US-09-131-551-11
;; Sequence 11, Application US/0913151
;; Publication No. US20010009667A1
;; GENERAL INFORMATION:
;; APPLICANT: BRUST, Stefan
;; APPLICANT: KNAPP, Stefan

;; APPLICANT: GERKEN, Manfred
;; APPLICANT: GUERTLER, Lutz
;; TITLE OF INVENTION: Peptides derived from a retrovirus of
;; TITLE OF INVENTION: the HIV group, and their use
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/131,551
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/394,021
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SANDERCOCK, Colin G.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 58315/106/BEAK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 145 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
US-09-131-551-11

Query Match 100.0%; Score 36; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 3e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQKQKNEQELLELDKQWASLNNWF 36
|||||
Db 106 YNTYITLLEESNQKQKNEQELLELDKQWASLNNWF 141

RESULT 12

US-10-000-321-11
;; Sequence 11, Application US/10000321
;; Publication No. US20020123039A1
;; GENERAL INFORMATION:
;; APPLICANT: BRUST, Stefan
;; APPLICANT: KNAPP, Stefan
;; GERKEN, Manfred
;; GUERTLER, Lutz
;; TITLE OF INVENTION: Peptides derived from a retrovirus of
;; TITLE OF INVENTION: the HIV group, and their use
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/000,321
;; FILING DATE: 04-Dec-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/131,551
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SANDERCOCK, Colin G.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 58315/106/BEAK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 145 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-000-321-11
Query Match 100.0%; Score 36; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 3e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YNTNTYTLLEESQNOQEKNEQELLELDKWASLWNWP 36
DB 106 YNTNTYTLLEESQNOQEKNEQELLELDKWASLWNWP 141
RESULT 13
US-09-854-816-30
; Sequence 30, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovashnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881

;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 269 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-854-816-30
Query Match 100.0%; Score 36; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.2e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YNTNTYTLLEESQNOQEKNEQELLELDKWASLWNWP 36
DB 169 YNTNTYTLLEESQNOQEKNEQELLELDKWASLWNWP 204
RESULT 14
US-09-854-816-31
; Sequence 31, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovashnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 269 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-854-816-31
Query Match 100.0%; Score 36; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.2e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YNTNTYTLLEESQNOQEKNEQELLELDKWASLWNWP 36
DB 169 YNTNTYTLLEESQNOQEKNEQELLELDKWASLWNWP 204

RESULT 15
US-10-351-641-856
; Sequence 856, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 856
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-856

Query Match 88.9%; Score 32; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.4e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 IYTLLEESQNKQEKNEQELLELDKWSLWNWF 36
Db 5 IYTLLEESQNKQEKNEQELLELDKWSLWNWF 36

Search completed: March 6, 2006, 16:32:48
Job time : 97.3333 secs

US-11-084-858-11

Query Match 75.0%; Score 36; DB 7; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.6e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTTTITLLAESQKNEQELLELDKWSLWNWF 36
|||||
Db 106 YTTTITLLAESQKNEQELLELDKWSLWNWF 141

RESULT 2

US-10-841-956A-1
; Sequence 1, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; PRIOR FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-1

Query Match 75.0%; Score 27; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.7e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKNEQELLELDKWSLWNWF 36
|||||
Db 10 EESQKNEQELLELDKWSLWNWF 36

RESULT 3

US-11-029-003-1
; Sequence 1, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEL, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029,003
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539,207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487,964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469,600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-029-003-1

Query Match 75.0%; Score 27; DB 7; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.7e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKNEQELLELDKWSLWNWF 36
|||||
Db 10 EESQKNEQELLELDKWSLWNWF 36

RESULT 4

US-11-187-687-22
; Sequence 22, Application US/11187687
; Publication No. US20060019347A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Ho Sung
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Hays, Anna-Maria
; APPLICANT: Wilson, Troy E.
; APPLICANT: Litzinger, David C.
; APPLICANT: Mariani, Roberto
; APPLICANT: Kimmel, Bruce E.
; APPLICANT: Keefe, William M.
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
; TITLE OF INVENTION: Acids
; FILE REFERENCE: AMBX-0041.00US
; CURRENT APPLICATION NUMBER: US/11/187,687
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: 60/590,035
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: 60/659,709
; PRIOR FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-22

Query Match 75.0%; Score 27; DB 7; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.7e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKNEQELLELDKWSLWNWF 36
|||||
Db 10 EESQKNEQELLELDKWSLWNWF 36

RESULT 5

US-11-112-277-33
; Sequence 33, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T20 Analogue
; FEATURE:
; NAME/KEY: MOD_RES

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; LOCATION: 37
; OTHER INFORMATION: Xaa is Lys linked to ABERA-MEA
US-11-112-277-33

Query Match      75.0%; Score 27; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 9.9e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWSLWNWF 36
Db 10 EESQOQEKNEQELLELDKWSLWNWF 36

RESULT 6
US-11-089-426-10
; Sequence 10, Application US/11089426
; Publication No. US20050261229A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Wing
; APPLICANT: Wesolowski, John
; TITLE OF INVENTION: Fc Fusion Proteins For Enhancing the Immunogenicity of
; TITLE OF INVENTION: Protein and Peptide Antigens
; FILE REFERENCE: LEX-007
; CURRENT APPLICATION NUMBER: US/11/089,426
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US/09/621,268
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/144,965
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fused
; OTHER INFORMATION: polypeptide from pDC-muFC vector
US-11-089-426-10

Query Match      75.0%; Score 27; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWSLWNWF 36
Db 8 EESQOQEKNEQELLELDKWSLWNWF 34

RESULT 7
US-11-187-687-24
; Sequence 24, Application US/11187687
; Publication No. US20060019347A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Ho Sung
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Hays, Anna-Maria
; APPLICANT: Wilson, Troy E.
; APPLICANT: Litzynger, David C.
; APPLICANT: Mariani, Roberto
; APPLICANT: Kimmel, Bruce E.
; APPLICANT: Keefe, William M.
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
; FILE REFERENCE: AMBX-0041.000S
; CURRENT APPLICATION NUMBER: US/11/187,687
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: 60/590,035
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: 60/659,709
; PRIOR FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 28
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-24

Query Match      75.0%; Score 27; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWSLWNWF 36
Db 18 EESQOQEKNEQELLELDKWSLWNWF 44

RESULT 8
US-10-841-956A-4
; Sequence 4, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-841-956A-4

Query Match      75.0%; Score 27; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 6.6e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWSLWNWF 36
Db 241 EESQOQEKNEQELLELDKWSLWNWF 267

RESULT 9
US-10-841-956A-8
; Sequence 8, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
```

```
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-841-956A-8
```

```
Query Match 75.0%; Score 27; DB 6; Length 269;
Best Local Similarity 100.0%; Pred. No. 6.7e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 EESQOQEKNEQELLELDKWSLWNWF 36
Db 243 EESQOQEKNEQELLELDKWSLWNWF 269
```

RESULT 10

```
US-10-841-956A-5
; Sequence 5, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-841-956A-5
```

```
Query Match 75.0%; Score 27; DB 6; Length 270;
Best Local Similarity 100.0%; Pred. No. 6.7e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 EESQOQEKNEQELLELDKWSLWNWF 36
Db 10 EESQOQEKNEQELLELDKWSLWNWF 36
```

RESULT 11

```
US-10-841-956A-7
; Sequence 7, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
```

```
; SEQ ID NO 7
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-841-956A-7
```

```
Query Match 75.0%; Score 27; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 7e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 EESQOQEKNEQELLELDKWSLWNWF 36
Db 10 EESQOQEKNEQELLELDKWSLWNWF 36
```

RESULT 12

```
US-10-841-956A-6
; Sequence 6, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-841-956A-6
```

```
Query Match 75.0%; Score 27; DB 6; Length 282;
Best Local Similarity 100.0%; Pred. No. 7e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 EESQOQEKNEQELLELDKWSLWNWF 36
Db 256 EESQOQEKNEQELLELDKWSLWNWF 282
```

RESULT 13

```
US-10-841-956A-9
; Sequence 9, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
```

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 9

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Peptide

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: construct

US-10-841-956A-9

Query Match

Best Local Similarity 75.0%; Score 27; DB 6; Length 293;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWSLWNWF 36

Db 267 EESQNOQEKNEQELLELDKWSLWNWF 293

RESULT 14

US-11-053-100-27

; Sequence 27, Application US/11053100

; Publication No. US2005025554A1

; GENERAL INFORMATION:

; APPLICANT: CHILKOTI, Ashutosh

; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION

; FILE REFERENCE: 4176-101 CIP

; CURRENT APPLICATION NUMBER: US/11/053,100

; CURRENT FILING DATE: 2005-02-08

; PRIOR APPLICATION NUMBER: US 09/812,382

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 60/190,659

; PRIOR FILING DATE: 2000-03-20

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 27

; LENGTH: 354

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)..(354)

; OTHER INFORMATION: pET15b-ELP4-60-EK-T20 peptide

US-11-053-100-27

Query Match

Best Local Similarity 75.0%; Score 27; DB 7; Length 354;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWSLWNWF 36

Db 328 EESQNOQEKNEQELLELDKWSLWNWF 354

RESULT 15

US-11-053-100-36

; Sequence 36, Application US/11053100

; Publication No. US2005025554A1

; GENERAL INFORMATION:

; APPLICANT: CHILKOTI, Ashutosh

; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION

; FILE REFERENCE: 4176-101 CIP

; CURRENT APPLICATION NUMBER: US/11/053,100

; CURRENT FILING DATE: 2005-02-08

; PRIOR APPLICATION NUMBER: US 09/812,382

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 60/190,659

; PRIOR FILING DATE: 2000-03-20

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 36

; LENGTH: 356

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)..(356)

; OTHER INFORMATION: pET17b-ELP4-60-TEV(Q/Y)-T20 peptide

US-11-053-100-36

Query Match

Best Local Similarity 75.0%; Score 27; DB 7; Length 356;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWSLWNWF 36

Db 330 EESQNOQEKNEQELLELDKWSLWNWF 356

Search completed: March 6, 2006, 16:33:25

Job time : 10.3333 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:12:57 ; Search time 117.333 Seconds
(without alignments)
134.809 Million cell updates/sec

Title: US-09-809-060A-2
Perfect score: 36
Sequence: 1 YTWITLLEESNQKQKNEQELLELDKWSLWNWF 36

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	36	3 AAY89837	Aay89837 Core poly
2	36	100.0	36	4 AAB54786	Aab54786 HIV antiv
3	36	100.0	36	4 AAB92245	Aab92245 Virus rel
4	36	100.0	36	4 AAB78238	Aab78238 Core poly
5	36	100.0	36	4 AAB78237	Aab78237 Core poly
6	36	100.0	36	4 AAU70180	Aau70180 HIV viral
7	36	100.0	36	4 ABB02830	Abb02830 Viral cor
8	36	100.0	36	4 ABB01245	Abb01245 Viral DP1
9	36	100.0	36	4 ABB01244	Abb01244 Viral DP1
10	36	100.0	36	4 AAU13791	Aau13791 DP178-lik
11	36	100.0	36	4 AAU13790	Aau13790 DP178-lik
12	36	100.0	36	5 AAU18772	Aau18772 HIV gp41
13	36	100.0	36	5 ADE02850	Ade02850 Hybrid po
14	36	100.0	36	5 ADE02716	Ade02716 Hybrid po
15	36	100.0	36	6 ABO10164	Abol0164 HIV1-SF2
16	36	100.0	36	8 ADN06923	Adn06923 Peptide #
17	36	100.0	36	8 ADS87258	Ads87258 HIV1 gp4
18	36	100.0	36	9 ADY171493	Ady171493 HIV-1 tra
19	36	100.0	269	2 AAY22835	Aay22835 SEQ ID NO
20	36	100.0	269	2 AAY22834	Aay22834 SEQ ID NO
21	36	100.0	269	5 ABG68305	Abg68305 Envelope
22	36	100.0	269	5 ABG68306	Abg68306 Envelope
23	36	100.0	269	6 ABUS7712	Abu57712 Human imm
24	36	100.0	269	6 ABUS7713	Abu57713 Human imm

25	36	100.0	275	2 AAW33615	Aaw33615 SOD/env-5
26	36	100.0	275	3 AAY77309	Aay77309 HIV-1 env
27	36	100.0	275	6 ABUS7560	Abu57560 AIDS asso
28	36	100.0	275	6 ABUS7560	Abu57560 AIDS asso
29	36	100.0	700	2 AAR05795	Aar05795 HIV-1 aci
30	36	100.0	855	2 AAW53112	Aaw53112 ENV prote
31	36	100.0	855	3 AAY77298	Aay77298 HIV-1 (AT
32	36	100.0	855	3 AAY77302	Aay77302 HIV-1 (AT
33	36	100.0	855	6 ABUS7553	Abu57553 AIDS asso
34	36	100.0	855	6 ABUS7550	Abu57550 AIDS asso
35	36	100.0	855	6 ABUS7550	Abu57550 AIDS asso
36	36	100.0	855	6 ABUS7550	Abu57550 AIDS asso
37	36	100.0	855	8 ADO26144	Ado26144 HIV env p
38	36	100.0	855	9 ADX39689	Adx39689 HIV env p
39	36	100.0	860	2 AAW31284	Aaw31284 HIV-SF2 v
40	36	100.0	863	1 AAP61509	Aap61509 Sequence
41	36	100.0	863	2 AAR29706	Aar29706 env gene
42	36	100.0	863	5 AAE35790	Aae35790 ARV-2 (9B
43	35	97.2	842	8 ADM73868	Adm73868 HIV-1 pol
44	33	91.7	854	2 AAW43070	Aaw43070 HIV-1 gp1
45	32	88.9	36	3 AAY89446	Aay89446 Core poly

ALIGNMENTS

RESULT 1
AAY89837
ID AAY89837 standard; peptide; 36 AA.
AC AAY89837;
XX
XX 23-MAY-2000 (first entry)
XX
XX Core polypeptide fragment T No. 1406.
XX
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
XX Unidentified.
XX
XX WO9595615-A1.
XX
XX 25-NOV-1999.
XX
XX 20-MAY-1999; 99WO-US011219.
XX
XX 20-MAY-1998; 98US-00082279.
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
XX Disclosure; Page 45; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic

CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AY8651-Y90055 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQKQKNEQELLELDKQASLWNWF 36
 |||||
 Db 1 YNTNTYTLLEESQKQKNEQELLELDKQASLWNWF 36

RESULT 2
 AAB54786
 ID AAB54786 standard; peptide; 36 AA.
 AC AAB54786;
 XX
 DT 11-SEP-2003 (revised)
 DT 05-MAR-2001 (first entry)
 XX
 DE HIV antiviral activity exhibiting peptide SEQ ID NO:3.
 XX
 KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KW antifusogenic; mobile blood component; measles virus; MeV; SIV;
 KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
 KW human respiratory syncytial virus; human immunodeficiency virus; HIV.
 XX
 OS Human immunodeficiency virus 1.

XX WO200069902-A1.
 PN 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013651.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 XX
 DR WPI; 2001-007496/01.

XX A modified peptide and a reactive group which is reactive with amino
 PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.

XX Claim 6; Page 173; 211pp; English.
 PS
 XX The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to

CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX

SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQKQKNEQELLELDKQASLWNWF 36
 |||||
 Db 1 YNTNTYTLLEESQKQKNEQELLELDKQASLWNWF 36

RESULT 3
 AAB92245
 ID AAB92245 standard; peptide; 36 AA.

AC AAB92245;

XX 22-JUN-2001 (first entry)

DE Virus related peptide SEQ ID NO:1421.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

PN 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 662; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 36
DB 1 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 36

RESULT 4
AAB78238
ID AAB78238 standard; peptide; 36 AA.
XX
AC AAB78238;
XX
DT 19-APR-2001 (first entry)
XX
DE Core polypeptide T1406.
XX
KW Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
XX antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
XX fusion-related disorder; bacterial infection; viral infection.
XX
OS Unidentified.
XX
FN WO200103723-A1.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-US018772.
XX
PR 09-JUL-1999; 99US-00350641.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
DR WPI; 2001-147136/15.
XX
PT New hybrid polypeptide, useful for preventing, treating and diagnosing
XX e.g. viral infections, comprises an enhancer peptide linked to a core
XX polypeptide.
XX
PS Disclosure; Page 58; 15lpp; English.
XX
CC The present sequence is a core polypeptide which may be linked to an
XX enhancer peptide to form a novel hybrid polypeptide. The hybrid
XX polypeptide exhibits enhanced pharmacokinetic properties relative to
XX those exhibited by the core polypeptide when introduced into a living
XX system. It is used to increase the in vitro or ex vivo half-life of the
XX core polypeptide. The hybrid and core polypeptides can be used for
XX modulating fusogenic events and intracellular processes involving coiled-
XX coil peptide interactions. Other uses include preventing, treating and/or
XX diagnosing disorders involving fusion events (e.g. modulation of
XX neurotransmitter exchange and sperm-egg fusion), intracellular processes
XX involving coiled-coil peptides (e.g. bacterial infections) and viral
XX infections that involve cell-cell and/or virus-cell fusion (e.g. viral
XX infections caused by human immunodeficiency virus, respiratory syncytial
XX virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
XX polio virus). The enhancer peptide sequence increases the half-life and
XX reduces the clearance rate of therapeutic peptides, which increases their
XX efficacy and minimises the incidence and severity of adverse side
XX effects. In addition, this increases the sensitivity of the diagnostic
XX procedure in which they are used
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 36

DB 1 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 36

RESULT 5
AAB78237
ID AAB78237 standard; peptide; 36 AA.
XX
AC AAB78237;
XX
DT 19-APR-2001 (first entry)
XX
DE Core polypeptide T1405.
XX
KW Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
XX antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
XX fusion-related disorder; bacterial infection; viral infection.
XX
OS Unidentified.
XX
FN WO200103723-A1.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-US018772.
XX
PR 09-JUL-1999; 99US-00350641.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
DR WPI; 2001-147136/15.
XX
PT New hybrid polypeptide, useful for preventing, treating and diagnosing
XX e.g. viral infections, comprises an enhancer peptide linked to a core
XX polypeptide.
XX
PS Disclosure; Page 58; 15lpp; English.
XX
CC The present sequence is a core polypeptide which may be linked to an
XX enhancer peptide to form a novel hybrid polypeptide. The hybrid
XX polypeptide exhibits enhanced pharmacokinetic properties relative to
XX those exhibited by the core polypeptide when introduced into a living
XX system. It is used to increase the in vitro or ex vivo half-life of the
XX core polypeptide. The hybrid and core polypeptides can be used for
XX modulating fusogenic events and intracellular processes involving coiled-
XX coil peptide interactions. Other uses include preventing, treating and/or
XX diagnosing disorders involving fusion events (e.g. modulation of
XX neurotransmitter exchange and sperm-egg fusion), intracellular processes
XX involving coiled-coil peptides (e.g. bacterial infections) and viral
XX infections that involve cell-cell and/or virus-cell fusion (e.g. viral
XX infections caused by human immunodeficiency virus, respiratory syncytial
XX virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
XX polio virus). The enhancer peptide sequence increases the half-life and
XX reduces the clearance rate of therapeutic peptides, which increases their
XX efficacy and minimises the incidence and severity of adverse side
XX effects. In addition, this increases the sensitivity of the diagnostic
XX procedure in which they are used
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 36
DB 1 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 36

RESULT 6
AAU70190

ID AAU70180 standard; peptide; 36 AA.
 AC AAU70180;
 XX
 DT 14-FEB-2002 (first entry)
 DE HIV viral envelope protein stabilising peptide #2.
 DE Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;
 KW anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
 KW alpha-helical region; ectodomain.
 XX Homo sapiens.
 OS
 PN WO200170262-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-US008108.
 XX
 PR 17-MAR-2000; 2000US-0189981P.
 XX
 PA (PANA-) PANACOS PHARM INC.
 PI Wild CT, Allaway GP;
 XX
 DR WPI; 2001-626098/72.
 XX
 PT Immunogenic composition for inhibiting HIV infection, comprises viral
 PT envelope protein or its fragment exterior to viral membrane, a
 PT stabilising peptide, and, optionally, viral cell surface receptor or its
 PT fragment.
 PS Claim 6; Page 45; 84pp; English.
 XX
 CC The invention relates to methods of generating immunogens that elicit
 CC neutralising antibodies which target regions of viral envelope proteins
 CC such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-
 CC 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and
 CC AAU70677-AAU70743 represent stabilising peptides modelling the alpha-
 CC helical regions of the ectodomain of the HIV-1 transmembrane protein to
 CC stabilise fusion-active intermediate structures, which can be used as
 CC vaccine immunogens. Immunogenic compositions comprise a viral envelope
 CC protein or its fragment exterior to the viral membrane, a stabilising
 CC peptide to disrupt formation of structural intermediates necessary for
 CC viral fusion and entry, and optionally, a viral cell surface receptor or
 CC its fragment. The stabilising peptide is capable of associating with the
 CC envelope protein or its fragment to form a stabilised, fusion active
 CC structure. Antibody binding assays are used to determine the ability of
 CC immunogen vaccines to generate an immune response to various forms of
 CC envelope. Virus neutralisation assays can be used to characterise the
 CC antibody response raised against HIV-1 gp41 domains. The sequences and
 CC methods are useful for inhibiting HIV infection, for inducing an immune
 CC response in an animal and for raising antibodies
 XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 36; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWF 36
 Db 1 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWF 36
 RESULT 7
 ABB02830
 ID ABB02830 standard; peptide; 36 AA.
 XX
 AC ABB02830;
 XX
 DT 11-SEP-2003 (revised)

DT 06-AUG-2003 (revised)
 DT 03-JAN-2002 (first entry)
 XX
 DE Viral core polypeptide, SEQ ID NO: 1357.
 XX
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 KW infection.
 XX Viruses.
 OS
 PN WO200164013-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 07-FEB-2001; 2001WO-US003988.
 XX
 PR 29-FEB-2000; 2000US-00515965.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
 XX
 DR WPI; 2001-514829/56.
 XX
 PT Heptad repeat region peptide analogs useful for inhibiting virus/cells
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus
 PT infection.
 PS Disclosure; Page 524; 587pp; English.
 XX
 CC The invention relates to isolated analogues of the heptad repeat region
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
 CC regions of proteins interact non-covalently with each other and/or with
 CC peptides derived from them. This interaction is required for normal
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region
 CC peptide analogues may be used to inhibit respiratory syncytial virus
 CC (RSV) infection in a cell. They may also be used to inhibit HIV
 CC infection. The present sequence is a peptide provided in the
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
 CC 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 36; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWF 36
 Db 1 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWF 36
 RESULT 8
 ABB01245
 ID ABB01245 standard; peptide; 36 AA.
 XX
 AC ABB01245;
 XX
 DT 11-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 03-JAN-2002 (first entry)
 XX
 DE Viral DP178/107-like region peptide T1406.
 XX
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 KW infection.
 XX Viruses.
 OS

PN WO200164013-A2.
 PD 07-SEP-2001.
 XX 07-FEB-2001; 2001WO-US003988.
 XX 29-FEB-2000; 2000US-00515965.
 XX (TRIM-) TRIMERIS INC.
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
 XX WPI; 2001-514829/56.
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus
 PT infection.
 XX Disclosure; Page 58; 587pp; English.
 XX The invention relates to isolated analogues of the heptad repeat region
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
 CC regions of proteins interact non-covalently with each other and/or with
 CC peptides derived from them. This interaction is required for normal
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region
 CC peptide analogues may be used to inhibit respiratory syncytial virus
 CC (RSV) infection in a cell. They may also be used to inhibit HIV
 CC infection. The present sequence is a peptide provided in the
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
 CC 11-SEP-2003 to standardise OS field)
 XX SQ Sequence 36 AA;
 Query Match 100.0%; Score 36; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YNTNTYTLLEESQOQKNEQELLELDKWASLWNWF 36
 DB 1 YNTNTYTLLEESQOQKNEQELLELDKWASLWNWF 36
 RESULT 9
 ABB01244
 ID ABB01244 standard; peptide; 36 AA.
 XX AC ABB01244;
 XX 11-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 03-JAN-2002 (first entry)
 XX Viral DP178/107-like region peptide T1405.
 XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 KW infection.
 XX Viruses.
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal is substituted by Ac"
 FT Modified-site 36
 FT /note= "C-terminal amide"
 XX WO200164013-A2.
 PN 07-SEP-2001.
 PD 07-FEB-2001.
 XX 07-FEB-2001; 2001WO-US003988.
 PF

XX 29-FEB-2000; 2000US-00515965.
 XX (TRIM-) TRIMERIS INC.
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
 XX WPI; 2001-514829/56.
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus
 PT infection.
 XX Disclosure; Page 58; 587pp; English.
 XX The invention relates to isolated analogues of the heptad repeat region
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
 CC regions of proteins interact non-covalently with each other and/or with
 CC peptides derived from them. This interaction is required for normal
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region
 CC peptide analogues may be used to inhibit respiratory syncytial virus
 CC (RSV) infection in a cell. They may also be used to inhibit HIV
 CC infection. The present sequence is a peptide provided in the
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
 CC 11-SEP-2003 to standardise OS field)
 XX SQ Sequence 36 AA;
 Query Match 100.0%; Score 36; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YNTNTYTLLEESQOQKNEQELLELDKWASLWNWF 36
 DB 1 YNTNTYTLLEESQOQKNEQELLELDKWASLWNWF 36
 RESULT 10
 AAU13791
 ID AAU13791 standard; peptide; 36 AA.
 XX AC AAU13791;
 XX 21-NOV-2001 (first entry)
 DT DP178-like/DP107-like peptide T-1406.
 DE Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
 KW antifusogenic; antiviral; HIV transmission; mutant; mutein.
 XX Human immunodeficiency virus 1; isolate LAI.
 OS Synthetic.
 XX WO200151673-A2.
 PN 19-JUL-2001.
 XX 05-JUL-2000; 2000WO-US035727.
 PF 09-JUL-1999; 99US-00350841.
 XX (TRIM-) TRIMERIS INC.
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
 PI WPI; 2001-442157/47.
 XX Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.

Query Match 100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESQKQKNEQELLELDKQWASLWNWF 36
|||||
Db 1 YNTYITLLEESQKQKNEQELLELDKQWASLWNWF 36
|||||

RESULT 13
ADE02850
ID ADE02850 standard; peptide; 36 AA.
AC ADE02850;
XX
XX 29-JAN-2004 (first entry)
DT
DE Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1357.
XX
XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;
KW pharmacokinetic; fusogenic; insulin; diabetes.
XX
XX Unidentified.
OS
XX US6348568-B1.
PN
XX
XX 19-FEB-2002.
PD
XX
XX 20-MAY-1999; 99US-00315304.
PF
XX
XX 20-MAY-1998; 98US-00082279.
PR
XX
XX (TRIM-) TRIMERIS INC.
PA
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
PI
XX WPI; 2002-424396/45.
DR

XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral
XX activity, has enhancer peptide sequence derived from retroviral envelope
XX protein sequences linked to core polypeptide e.g. therapeutic protein.
XX
XX Disclosure; SEQ ID NO 1357; 70pp; English.

XX The invention relates to a novel hybrid polypeptide comprising an
XX enhancer peptide sequence linked to a core polypeptide. The enhancer
XX peptide sequence comprises QWEQKI or WASLWEP. The invention also
XX includes novel peptides that exhibit anti-fusogenic activity, antiviral
XX activity and/or ability to modulate intracellular processes. The novel
XX hybrid polypeptide has virucide and antidiabetic activity. The enhancer
XX peptide sequence enhances pharmacokinetic properties of any core
XX polypeptide, for example, a polypeptide useful for the treatment or
XX prevention of a disease, or an imaging agent useful for imaging
XX structures in vivo. The core polypeptides and hybrid polypeptides are
XX useful for modulating fusogenic events and exhibit antifusogenic or
XX antiviral activity. The novel hybrid polypeptide is useful for decreasing
XX viral infection and modulating intracellular processes involving coiled-
XX coil peptide interactions. The novel hybrid polypeptide comprises insulin
XX or its fragment, so the core polypeptide is useful for ameliorating the
XX symptoms of forms of diabetes. The novel hybrid polypeptide is also
XX useful as a part of prognosis for preventing disorders including fusion
XX events and viral infection that involves cell-cell and/or virus-cell
XX fusion, and for diagnosis and in vivo imaging methods. This sequence
XX represents an enhancer peptide of the invention.

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESQKQKNEQELLELDKQWASLWNWF 36
|||||

Db 1 YNTYITLLEESQKQKNEQELLELDKQWASLWNWF 36

RESULT 14

ADE02716
ID ADE02716 standard; peptide; 36 AA.
XX
AC ADE02716;

XX
XX 29-JAN-2004 (first entry)
DT
DE Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1223.
XX
XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;
KW pharmacokinetic; fusogenic; insulin; diabetes.
XX
XX Unidentified.

XX Key Location/Qualifiers
PH Modified-site 1
FT Modified-site 36 /note= "Residue is modified by acetyl group"
FT Modified-site 36 /note= "C-terminal amide"
XX
XX US6348568-B1.
PN
XX
XX 19-FEB-2002.
PD
XX
XX 20-MAY-1999; 99US-00315304.
PF
XX
XX 20-MAY-1998; 98US-00082279.
PR
XX
XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
PI
XX WPI; 2002-424396/45.
DR
XX
XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral
XX activity, has enhancer peptide sequence derived from retroviral envelope
XX protein sequences linked to core polypeptide e.g. therapeutic protein.
XX
XX Disclosure; SEQ ID NO 1223; 70pp; English.

XX The invention relates to a novel hybrid polypeptide comprising an
XX enhancer peptide sequence linked to a core polypeptide. The enhancer
XX peptide sequence comprises QWEQKI or WASLWEP. The invention also
XX includes novel peptides that exhibit anti-fusogenic activity, antiviral
XX activity and/or ability to modulate intracellular processes. The novel
XX hybrid polypeptide has virucide and antidiabetic activity. The enhancer
XX peptide sequence enhances pharmacokinetic properties of any core
XX polypeptide, for example, a polypeptide useful for the treatment or
XX prevention of a disease, or an imaging agent useful for imaging
XX structures in vivo. The core polypeptides and hybrid polypeptides are
XX useful for modulating fusogenic events and exhibit antifusogenic or
XX antiviral activity. The novel hybrid polypeptide is useful for decreasing
XX viral infection and modulating intracellular processes involving coiled-
XX coil peptide interactions. The novel hybrid polypeptide comprises insulin
XX or its fragment, so the core polypeptide is useful for ameliorating the
XX symptoms of forms of diabetes. The novel hybrid polypeptide is also
XX useful as a part of prognosis for preventing disorders including fusion
XX events and viral infection that involves cell-cell and/or virus-cell
XX fusion, and for diagnosis and in vivo imaging methods. This sequence
XX represents an enhancer peptide of the invention.

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESQKQKNEQELLELDKQWASLWNWF 36
|||||

Search completed: March 6, 2006, 16:19:04
Job time : 118.333 secs

Db 1 YNTIYTLLESQOQEKNEQELLELDKWASLWNWF 36

RESULT 15

ABO10164
ID ABO10164 standard; peptide; 36 AA.

XX AC ABO10164;

XX 23-OCT-2003 (revised)
DT 19-AUG-2003 (first entry)

XX HIV1-SF2 gp41 protein, DP85 peptide.

XX HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.

XX Human immunodeficiency virus 1; isolate SF2.

XX US6518013-B1.

XX 11-FEB-2003.

XX 07-JUN-1995; 95US-00485546.

XX 07-JUN-1993; 93US-00073028.

PR 07-JUN-1994; 94US-00255208.

PR 20-DEC-1994; 94US-00360107.

XX (TRIM-) TRIMERIS INC.

XX Barney SO, Lambert DM, Petteway SR;

XX WPI; 2003-465599/44.

PT Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
PT the cell with a peptide consisting of a region of Epstein-Barr virus
PT protein.

XX Example; Fig 1; 716pp; English.

CC The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective
CC concentration of a peptide consisting of a region of 16-39 consecutive
CC amino acids of an Epstein-Barr virus protein for an effective period of
CC time, where the region is recognised by one or more of ALWM015,
CC 107x178x4 or PLZIP sequence search motifs, the peptide further comprises
CC an amino terminal X, and a carboxy terminal Z in which X comprises an
CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
CC group or macromolecular carrier group, and Z comprises a carboxyl group,
CC amido group, hydrophobic group, or macromolecular carrier group, and
CC fusion of the virus to the cell is inhibited. The peptides were
CC identified by analysing the structure/motifs present in the HIV-1
CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
CC motif containing peptides were used to design the motifs cited above,
CC which in turn were used to analyse proteins from other pathogenic
CC organisms and HIV isolates, looking for DP107/178 structural analogues.
CC The method is useful for inhibiting transmission of Epstein-Barr virus to
CC a cell and Epstein-Barr virus infection. The present sequence is a
CC control peptide used in the study of the DP178 structure. (Updated on 23-
CC OCT-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. NO. 3.3e-27;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQOQEKNEQELLELDKWASLWNWF 36

|||||

Db 1 YNTIYTLLESQOQEKNEQELLELDKWASLWNWF 36

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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:50:56 ; Search time 10 Seconds
(without alignments)
72.002 Million cell updates/sec

Title: US-09-809-060A-2
Perfect score: 198
Sequence: 1 YNTYITLLEESQNOEKNEQELLELDKQASLWNWF 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 78453

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Published Applications AA New.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	88.9	36	US-10-841-956A-1	Sequence 1, Appli
2	176	88.9	36	US-11-029-003-1	Sequence 1, Appli
3	176	88.9	36	US-11-187-687-22	Sequence 22, Appli
4	176	88.9	37	US-11-112-277-33	Sequence 33, Appli
5	176	88.9	44	US-11-187-687-24	Sequence 24, Appli
6	164	82.8	44	US-11-089-426-10	Sequence 10, Appli
7	138	69.7	36	US-10-506-796A-7	Sequence 7, Appli
8	137	69.2	36	US-10-506-796A-5	Sequence 5, Appli
9	135	68.2	35	US-10-506-796A-1	Sequence 1, Appli
10	135	68.2	36	US-10-506-796A-3	Sequence 3, Appli
11	133	67.2	36	US-10-506-796A-6	Sequence 6, Appli
12	124	62.6	39	US-10-841-956A-3	Sequence 3, Appli
13	124	62.6	39	US-11-029-003-3	Sequence 3, Appli
14	124	62.6	40	US-11-112-277-34	Sequence 34, Appli
15	123	62.1	36	US-10-506-796A-4	Sequence 4, Appli
16	104	52.5	38	US-11-151-598-4	Sequence 4, Appli
17	99	50.0	34	US-11-112-277-6	Sequence 6, Appli
18	99	50.0	34	US-11-112-277-38	Sequence 38, Appli
19	99	50.0	34	US-11-151-598-10	Sequence 10, Appli
20	99	50.0	34	US-11-151-598-12	Sequence 12, Appli
21	99	50.0	35	US-11-112-277-7	Sequence 7, Appli
22	99	50.0	35	US-11-112-277-37	Sequence 37, Appli
23	99	50.0	47	US-11-151-598-5	Sequence 5, Appli
24	97	49.0	34	US-11-112-277-8	Sequence 8, Appli
25	97	49.0	34	US-11-112-277-36	Sequence 36, Appli

26 89 44.9 15 7 US-11-045-024-13381. Sequence 13381, A
27 80 40.4 15 7 US-11-045-024-13388. Sequence 13388, A
28 79 39.9 15 7 US-11-045-024-12922. Sequence 12922, A
29 73 36.9 15 7 US-11-045-024-13379. Sequence 13379, A
30 72 36.4 11 7 US-11-045-024-8659. Sequence 8659, Ap
31 71 35.9 11 7 US-11-045-024-103. Sequence 103, App
32 71 35.9 11 7 US-11-045-024-3968. Sequence 3968, Ap
33 71 35.9 11 7 US-11-045-024-7039. Sequence 7039, Ap
34 68 34.3 10 7 US-11-045-024-5568. Sequence 5568, Ap
35 66 33.3 11 7 US-11-045-024-102. Sequence 102, App
36 66 33.3 11 7 US-11-045-024-3967. Sequence 3967, Ap
37 66 33.3 11 7 US-11-045-024-6943. Sequence 6943, Ap
38 64 32.3 35 7 US-11-112-277-40. Sequence 40, Appl
39 64 32.3 36 7 US-11-112-277-39. Sequence 39, Appl
40 62 31.3 9 7 US-11-045-024-3776. Sequence 3776, Ap
41 62 31.3 9 7 US-11-045-024-5533. Sequence 5533, Ap
42 62 31.3 9 7 US-11-045-024-12581. Sequence 12581, A
43 62 31.3 11 7 US-11-045-024-101. Sequence 101, App
44 62 31.3 11 7 US-11-045-024-3966. Sequence 3966, Ap
45 62 31.3 11 7 US-11-045-024-3969. Sequence 3969, Ap

ALIGNMENTS

RESULT 1
US-10-841-956A-1
; Sequence 1, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-1

Query Match 88.9%; Score 176; DB 6; Length 36;
Best Local Similarity 86.1%; Pred. No. 1.7e+15;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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Db 1 YTSLSHLSLEESQNOEKNEQELLELDKQASLWNWF 36
||:|||||

RESULT 2
US-11-029-003-1
; Sequence 1, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEL, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029,003
; CURRENT FILING DATE: 2005-01-05


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FILE REFERENCE: 500862003700
CURRENT APPLICATION NUMBER: US/11/112,277
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/565,228
PRIOR FILING DATE: 2004-04-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: T1249 Analogue
NAME/KEY: MOD_RES
LOCATION: 40
OTHER INFORMATION: Xaa is Lys linked to ABEA-MPA
US-11-112-277-34

Query Match          62.6%; Score 124; DB 7; Length 40;
Best Local Similarity 71.9%; Pred. No. 4.2e-09;
Matches 23; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Db 8 ITALLEQAQIQEKKNEYELQKLDKWASLWNWF 39

RESULT 15
US-10-506-796A-4
Sequence 4, Application US/10506796A
Publication No. US20060013831A1
GENERAL INFORMATION:
APPLICANT: MOR, Tsafirir
APPLICANT: MATOBA, Nobuyuki
APPLICANT: ARNTZEN, Charles
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
FILE REFERENCE: 01231.000602
CURRENT APPLICATION NUMBER: US/10/506,796A
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: PCT/US03/07073
PRIOR FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: 60/362,247
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 36
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(35)
OTHER INFORMATION: HIV-1 isolate MN clone v5 (residues 649-685)
US-10-506-796A-4

Query Match          62.1%; Score 123; DB 6; Length 36;
Best Local Similarity 88.0%; Pred. No. 5e-09;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 SQTQEKNEQELGLDKWESLWNWF 25

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GenCore version 5.1.7
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Perfect score: 198
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	198	100.0	36	4	US-10-252-136-3
3	198	100.0	36	4	US-10-351-641-1357
4	198	100.0	36	4	US-10-267-682-3
5	198	100.0	36	4	US-10-267-748-3
6	198	100.0	36	4	US-10-663-589-38
7	198	100.0	36	4	US-10-671-282-38
8	198	100.0	36	5	US-10-168-295-3
9	198	100.0	36	5	US-10-950-010-3
10	198	100.0	36	6	US-11-066-697-1421
11	187	94.4	36	4	US-10-351-641-1051
12	185	93.4	36	3	US-09-809-060-22
13	185	93.4	36	3	US-09-779-451-47
14	185	93.4	36	4	US-10-351-641-856
15	185	93.4	36	4	US-10-685-801-47
16	185	93.4	36	4	US-10-660-206-47
17	185	93.4	46	3	US-09-809-060-20
18	185	93.4	46	3	US-09-779-451-45
19	185	93.4	46	4	US-10-685-801-45
20	185	93.4	46	4	US-10-660-206-45
21	183	92.4	46	3	US-09-854-816-109
22	181	91.4	36	4	US-10-351-641-642
23	181	91.4	36	4	US-10-457-780-52
24	181	91.4	36	5	US-10-950-010-535
25	181	91.4	36	5	US-10-950-010-537
26	180	90.9	36	5	US-10-950-010-540
27	178	89.9	36	3	US-09-809-060-3

28	178	89.9	36	4	US-10-252-136-4	Sequence 4, Appli
29	178	89.9	36	4	US-10-351-641-1358	Sequence 1358, Ap
30	178	89.9	36	4	US-10-351-641-1359	Sequence 1359, Ap
31	178	89.9	36	4	US-10-267-682-4	Sequence 4, Appli
32	178	89.9	36	4	US-10-267-748-4	Sequence 4, Appli
33	178	89.9	36	4	US-10-663-589-39	Sequence 39, Appl
34	178	89.9	36	4	US-10-671-282-39	Sequence 39, Appl
35	178	89.9	36	5	US-10-168-295-4	Sequence 4, Appli
36	178	89.9	36	5	US-10-950-010-4	Sequence 541, App
37	178	89.9	36	5	US-10-950-010-541	Sequence 541, App
38	178	89.9	36	6	US-11-066-697-1422	Sequence 1422, Ap
39	177	89.4	36	4	US-10-351-641-1515	Sequence 1515, Ap
40	176	88.9	36	3	US-09-809-060-1	Sequence 1, Appli
41	176	88.9	36	3	US-09-809-060-85	Sequence 85, Appl
42	176	88.9	36	3	US-09-796-202-10	Sequence 10, Appl
43	176	88.9	36	3	US-09-960-717-2	Sequence 2, Appli
44	176	88.9	36	3	US-09-779-451-5	Sequence 5, Appli
45	176	88.9	36	3	US-09-834-628-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-809-060-2
; Sequence 2, Application US/09809060
; Publication NO. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Willd, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; TITLE OF INVENTION: Regions of HIV Envelope Proteins
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-2

Query Match 100.0%; Score 198; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YNTIYTLLEESQNOQKNEQELLELDKWASLWNWF 36
DB 1 YNTIYTLLEESQNOQKNEQELLELDKWASLWNWF 36

RESULT 2
US-10-252-136-3
; Sequence 3, Application US/10252136
; Publication NO. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

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; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-3

Query Match          100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 3
US-10-351-641-1357
; Sequence 1357, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M. D.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1357
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1357

Query Match          100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 4
US-10-267-682-3
; Sequence 3, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-267-682-3

Query Match          100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 5
US-10-267-748-3
; Sequence 3, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
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34

FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
APPLICATION DATA:
PRIORITY NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-267-748-3

Query Match 100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YNTIYTLLEESQNOQKNEQELLELDKWSLWNNWF 36

RESULT 6
US-10-663-589-38
Sequence 38, Application US/10663589
Publication No. US20040063637A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
TITLE OF INVENTION: gp41-derived peptides, and its use in therapy
FILE REFERENCE: TRM-003
CURRENT APPLICATION NUMBER: US/10/663,589
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 60/414,441
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn version 3.2
SEQ ID NO 38
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-663-589-38

Query Match 100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YNTIYTLLEESQNOQKNEQELLELDKWSLWNNWF 36

RESULT 7
US-10-671-282-38
Sequence 38, Application US/10671282
Publication No. US20040122214A1
GENERAL INFORMATION:
APPLICANT: Trimeris, Inc.
TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
TITLE OF INVENTION: their use in therapy
FILE REFERENCE: TRM-004

35

CURRENT APPLICATION NUMBER: US/10/671,282
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: 60/414,439
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn version 3.2
SEQ ID NO 38
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthesized
US-10-671-282-38

Query Match 100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQKNEQELLELDKWSLWNNWF 36
DB 1 YNTIYTLLEESQNOQKNEQELLELDKWSLWNNWF 36

RESULT 8
US-10-168-295-3
Sequence 3, Application US/10168295
Publication No. US20050065319A1
GENERAL INFORMATION:
APPLICANT: Baroudy, Bahige M.
TITLE OF INVENTION: Combination Method For Treating Viral Infections
FILE REFERENCE: IN01358
CURRENT APPLICATION NUMBER: US/10/168,295
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: PCT/US01/48802
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,657
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 36
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-3

Query Match 100.0%; Score 198; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQKNEQELLELDKWSLWNNWF 36
DB 1 YNTIYTLLEESQNOQKNEQELLELDKWSLWNNWF 36

RESULT 9
US-10-950-010-3
Sequence 3, Application US/10950010
Publication No. US20050070475A1
GENERAL INFORMATION:
APPLICANT: BRIDON, Dominique P.
APPLICANT: DUFRESNE, Robert S.
APPLICANT: BOUDJELILAB, Nissab
APPLICANT: ROBITAILLE, Martin
APPLICANT: MILNER, Peter G.
TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL
TITLE OF INVENTION: INFECTION
FILE REFERENCE: 500862001501/REDC-1512
CURRENT APPLICATION NUMBER: US/10/950,010
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: US 09/623,533
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/US00/13651
FILE REFERENCE: 2000-05-17


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; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0.
; SEQ ID NO 47
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus t
; US-09-779-451-47

```

Query Match 93.4%; Score 185; DB 3; Length 36;
Best Local Similarity 91.7%; Pred. No. 2.2e-14;
Matches 33; Conservative 2; Mismatches 1; Indels

[illegible]

RESULT 14

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US/10-351-641-856
; Sequence 856, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES W
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 856
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-856

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Query Match	93.4%;	Score 185;	DB 4;	Length 36;
Best Local Similarity	94.4%;	Pred. No. 2.2e-14;		
Matches 34;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;			

Qy

1 YNTIYTLLEESQNQQEKNEQELLELDKWSLWNWF 36
|| |||

Db

1 YTKFYITLLLEESNQOOEKNEQELLELDKWSLWNWF 36

RESULT 15

US-10-685-801-47
; Sequence 47, Application US/10685801
; Publication NO. US20040132011A1
; GENERAL INFORMATION:
; APPLICANT: Allaway, Graham P.
; APPLICANT: Wild, Carl T.
; APPLICANT: Salzwedel, Karl
; TITLE OF INVENTION: Method for Detecting Viral Inactivating Agents

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:37:45 ; Search time 18.3333 Seconds
(without alignments)
188.935 Million cell updates/sec

Title: US-09-809-060A-2
Perfect score: 198
Sequence: 1 YNTIYTLLEESQKQKNEQELLELDKWLWVWF 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	21.2	36	2 D83682	hypothetical prote
2	41	20.7	41	2 S27169	aralkyl-CoA N-acyl
3	39	19.7	46	2 B30474	homeotic protein H
4	39	19.7	50	2 D89972	hypothetical prote
5	39	19.7	50	2 F86472	5.7K hypothetical
6	38	19.2	43	2 S02031	zinc-binding prote
7	38	19.2	50	2 T14888	hypothetical prote
8	37	18.7	41	2 T48342	hypothetical prote
9	36	18.2	24	2 S01808	hemoglobin AII - t
10	36	18.2	30	2 I77411	renin-2 - mouse (f
11	36	18.2	32	2 I46523	troponin T 4f - ra
12	36	18.2	45	2 S01814	hemoglobin BII - t
13	36	18.2	48	2 F85646	hypothetical prote
14	35.5	17.9	49	2 S39957	ribosomal protein
15	35	17.7	30	2 A34461	heat shock protein
16	35	17.7	33	2 A82186	hypothetical prote
17	35	17.7	38	2 I66797	troponin T 3f - ra
18	35	17.7	42	2 T07291	hypothetical prote
19	35	17.7	47	2 A40703	androgen-binding p
20	35	17.7	48	2 S74261	troponin T3f, fast
21	35	17.7	50	2 T06541	probable NADPH-fer
22	34	17.2	39	2 I54059	Na+/K+-exchanging
23	34	17.2	49	2 T06923	high light-inducib
24	33.5	16.9	36	2 A95135	hypothetical prote
25	33.5	16.9	45	2 C82233	hypothetical prote
26	33.5	16.9	47	2 S31005	gene 60 protein -
27	33.5	16.9	47	2 G84063	hypothetical prote
28	33	16.7	26	2 S27170	aralkyl-CoA N-a
29	33	16.7	36	2 A34594	myosin regulatory

30	33	16.7	43	2 S21282	thymosin beta-11 -
31	33	16.7	43	2 H83653	hypothetical prote
32	33	16.7	44	1 RH805	somatomedin - bo
33	33	16.7	49	2 AG3362	hypothetical prote
34	32.5	16.4	43	2 B83894	hypothetical prote
35	32.5	16.4	46	2 A95010	hypothetical prote
36	32.5	16.4	46	2 C95173	hypothetical prote
37	32.5	16.4	49	2 A37405	androgen-binding p
38	32	16.2	29	2 E64036	hypothetical prote
39	32	16.2	30	2 H70152	hypothetical prote
40	32	16.2	39	2 C95128	hypothetical prote
41	32	16.2	42	2 T13295	hypothetical prote
42	32	16.2	43	2 T07503	hypothetical prote
43	32	16.2	44	2 E95248	hypothetical prote
44	32	16.2	44	2 C34327	troponin T, fast s
45	32	16.2	45	1 EABP59	early protein gp5

ALIGNMENTS

RESULT 1

D83682
hypothetical protein BH0260 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: D83682
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83682
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <STO>
A;Cross-references: UNIPROT:Q9KG53; UNIPARC:UPI0000139521; GB:AP001507; GB:BA000004; NID
A;Experimental source: strain C-125
C:Genetics:
A;Gene: BH0260

Query Match 21.2%; Score 42; DB 2; Length 36;
Best Local Similarity 47.6%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY	8	LEESQKQKNEQELLELDK 28
		:
DB	4	LVNESWEQQRKKIQLLSDEK 24

RESULT 2

S27169
aralkyl-CoA N-acyltransferase (EC 2.3.1.-) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Mar-1997 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: S27169
R;Kelley, M.; Vessey, D.A.
Biochem. J. 288, 315-317, 1992
A;Title: Structural comparison between the mitochondrial aralkyl-CoA and arylacetyl-CoA
A;Reference number: S27169; MUID:93075097; PMID:1445276
A;Accession: S27169
A;Molecule type: protein
A;Residues: 1-41 <REL>
A;Cross-references: UNIPROT:Q9T209; UNIPARC:UPI000008C6A3
A;Experimental source: kidney
C:Keywords: acyltransferase

Query Match 20.7%; Score 41; DB 2; Length 41;
Best Local Similarity 47.1%; Pred. No. 1.8e+02;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY	1	YNTIYTLLEESQKQK 17
DB	23	YNTYHYVEDLNKQGE 39

```

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F86472
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <STO>
A;Cross-references: UNIPROT:Q9C6E9; UNIPARC:UPI00000A80F1; GB:AE005172; NID:G11386311;
C;Genetics:
A;Map position: 1

Query Match 19.7%; Score 39; DB 2; Length 50;
Best Local Similarity 44.4%; Pred. No. 3.8e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELD 27
Db 20 EESQTESESEDETESD 37

RESULT 6
S02031
zinc-binding protein - rat (tentative sequence) (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Accession: S02031
R;Brand, I.A.; Heinzel, A.; Kratzin, H.; Soeling, H.D.
Eur. J. Biochem. 177, 561-568, 1988
A;Title: Properties of a 19-kDa Zn(2+)-binding protein and sequence of the Zn(2+)-binding
A;Reference number: S02031; MUID:89064809; PMID:3197718
A;Accession: S02031
A;Molecule type: protein
A;Residues: 1-43 <BRA>
A;Cross-references: UNIPARC:UPI0000176609
C;Superfamily: prothymosin alpha
C;Keywords: zinc

Query Match 19.2%; Score 38; DB 2; Length 43;
Best Local Similarity 38.9%; Pred. No. 4.2e+02;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 8 LLEESQNOQEKNEQELLE 25
Db 2 VVEEENGAESEETAE 19

RESULT 7
T14888
hypothetical protein - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14888
R;Wong, K.K.; McClelland, M.; Stillwell, L.C.; Siak, E.C.; Thurston, S.J.; Saffer, J.D.
Infect. Immun. 66, 3365-3371, 1998
A;Title: Identification and sequence analysis of a 27-kilobase chromosomal fragment con-
ovar typhimurium LT2.
A;Reference number: Z18249; MUID:98298059; PMID:9632606
A;Accession: T14888
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-50 <WON>
A;Cross-references: UNIPROT:O85329; UNIPARC:UPI00000B3232; EMBL:AF060869; NID:G3323584;
C;Genetics:
A;Gene: yJcC
A;Map position: 92 min
C;Superfamily: probable membrane protein ylaB

Query Match 19.2%; Score 38; DB 2; Length 50;
Best Local Similarity 46.7%; Pred. No. 5e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TWTIYTLLEESQNOQ 16

homeotic protein Hox 1.3 homolog - sheep (fragment)
B30474
N;Alternate names: homeotic protein Ohox-8-1
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
C;Accession: B30474
R;Choi, C.L.; Hudson, P.; Stauder, A.; Pietersz, G.; Brandon, M.
Gene 63, 187-197, 1998
A;Title: Molecular cloning and characterization of ovine homeo-box-containing genes.
A;Reference number: JT0273; MUID:88255866; PMID:2898416
A;Accession: B30474
A;Molecule type: DNA
A;Residues: 1-46 <CHO>
A;Cross-references: UNIPARC:UPI000017A32E
A;Note: the authors translated the codon TCC for residue 3 as Pro, CAG for residue 42 as
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;11-46/Domain: homeobox homology (fragment) <HOX>

Query Match 19.7%; Score 39; DB 2; Length 46;
Best Local Similarity 34.6%; Pred. No. 3.5e+02;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 3 NTIYTLLEESQNOQEKNEQELLELDK 28
Db 2 NSNYTGEPKRSRTATYRQVLELEK 27

RESULT 4
D89972
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89972
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc-
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89972
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <KUR>
A;Cross-references: UNIPROT:Q99T25; UNIPARC:UPI00000D7729; GB:BA000018; PID:G13701646;
A;Experimental source: strain N315
C;Genetics:
A;Gene: SAS053

Query Match 19.7%; Score 39; DB 2; Length 50;
Best Local Similarity 70.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 QNOQEKNEOS 22
Db 38 QNDQEKNSSE 47

RESULT 5
F86472
5.7K hypothetical protein T3209.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86472
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunt, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
```

```
Db          16 TMTFFSLSEQAQDQ 30

RESULT 8
T48342
hypothetical protein F15A17.240 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48342
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24491
A:Accession: T48342
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-41 <BR>
A:Cross-references: UNIPROT:Q9LYW4; UNIPARC:UPI00000AA77A; EMBL:AL163002
A:Experimental source: cultivar Columbia; BAC clone F15A17
C:Genetics:
A:Map position: 5
A:Note: F15A17.240

Query Match      18.7%; Score 37; DB 2; Length 41;
Best Local Similarity 37.5%; Pred. No. 5.2e+02;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 TLTESQOQEKNEQE 22
|:|:|:|:|:|:|
|:|:|:|:|:|:|
Db 22 TLEGGTEEDNEQE 37

RESULT 9
S01808
hemoglobin AII - tube worm (Lamellibrachia sp.) (fragment)
C:Species: Lamellibrachia sp.
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: S01808
R:Suzuki, T.; Takagi, T.; Ohta, S.
Biochem. J. 255, 541-545, 1988
A:Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably
A:Reference number: S01807; MUID:89076216; PMID:3202832
A:Accession: S01808
A:Molecule type: protein
A:Residues: 1-24 <SUZ>
A:Cross-references: UNIPROT:Q9TWS6; UNIPARC:UPI000017711B
C:Keywords: oxygen carrier

Query Match      18.2%; Score 36; DB 2; Length 24;
Best Local Similarity 26.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 8; Mismatches 2; Indels 4; Gaps 1;

QY 16 QEKNEQELLEDKWASLWN 34
|:|:|:|:|:|:|
|:|:|:|:|:|:|
Db 8 EDRREMQLM----WANVWS 22

RESULT 10
I77411
renin-2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C:Accession: I77411
R:Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.W.
Mol. Cell. Biol. 4, 2321-2331, 1984
A:Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analysis
A:Reference number: I57576; MUID:85085936; PMID:6392850
A:Accession: I77411
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-30 <RES>
A:Cross-references: UNIPROT:P00796; UNIPARC:UPI000016C94B; GB:K02801; NID:g200695; PIDN:
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C:Superfamily: Pepsin

Query Match      18.2%; Score 36; DB 2; Length 30;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 WASLWNW 35
|:|:|:|:|
|:|:|:|:|
Db 9 WALLWLW 15

RESULT 11
I46523
troponin T 4f - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
C:Accession: I46523
R:Briggs, M.M.; Lin, J.J.; Schachar, F.H.
J. Muscle Res. Cell. Motil. 8, 1-12, 1987
A:Title: The extent of amino-terminal heterogeneity in rabbit fast skeletal muscle tropo
A:Reference number: I46522; MUID:87251333; PMID:2439538
A:Accession: I46523
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-32 <BRI>
A:Cross-references: UNIPARC:UPI000016C510; EMBL:U04978; NID:g440816; PIDN:AAA16031.1; PI
C:Superfamily: troponin T

Query Match      18.2%; Score 36; DB 2; Length 32;
Best Local Similarity 46.2%; Pred. No. 5.2e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQE 22
|:|:|:|:|:|:|
|:|:|:|:|:|:|
Db 11 EEAQEEVEHEE 23

RESULT 12
S01814
hemoglobin BII - tube worm (Lamellibrachia sp.) (fragment)
C:Species: Lamellibrachia sp.
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-May-2004
C:Accession: S01814
R:Suzuki, T.; Takagi, T.; Ohta, S.
Biochem. J. 255, 541-545, 1988
A:Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably
A:Reference number: S01807; MUID:89076216; PMID:3202832
A:Accession: S01814
A:Molecule type: protein
A:Residues: 1-45 <SUZ>
A:Cross-references: UNIPARC:UPI000017711A
C:Keywords: oxygen carrier

Query Match      18.2%; Score 36; DB 2; Length 45;
Best Local Similarity 26.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 8; Mismatches 2; Indels 4; Gaps 1;

QY 16 QEKNEQELLEDKWASLWN 34
|:|:|:|:|:|:|
|:|:|:|:|:|:|
Db 8 EDRREMQLM----WANVWS 22

RESULT 13
F85646
hypothetical protein Z1518 [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85646
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
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*T 0 1.0

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:31:26 ; Search time 114.667 Seconds
(without alignments)
137.945 Million cell updates/sec

Title: US-09-809-060A-2

Perfect score: 198

Sequence: 1 YNTIYTLLESQKQKNEQLLELDKWLWNP 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Genesecp1980s:*
- 2: Genesecp1990s:*
- 3: Genesecp2000s:*
- 4: Genesecp2001s:*
- 5: Genesecp2002s:*
- 6: Genesecp2003as:*
- 7: Genesecp2003bs:*
- 8: Genesecp2004s:*
- 9: Genesecp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	36	3 AAY89837	Aay89837 Core poly
2	198	100.0	36	4 AAB54786	Aab54786 HIV antiv
3	198	100.0	36	4 AAB92245	Aab92245 Virus rel
4	198	100.0	36	4 AAB78238	Aab78238 Core poly
5	198	100.0	36	4 AAB78237	Aab78237 Core poly
6	198	100.0	36	4 AAU70180	Aau70180 HIV viral
7	198	100.0	36	4 ABB02830	Abb02830 Viral cor
8	198	100.0	36	4 ABB01245	Abb01245 Viral DP1
9	198	100.0	36	4 ABB01244	Abb01244 Viral DP1
10	198	100.0	36	4 AAU13791	Aau13791 DP178-lik
11	198	100.0	36	4 AAU13790	Aau13790 DP178-lik
12	198	100.0	36	5 AAO18772	Aao18772 HIV gp41
13	198	100.0	36	5 ADE02850	Ade02850 Hybrid po
14	198	100.0	36	5 ADE02716	Ade02716 Hybrid po
15	198	100.0	36	6 ABO10164	Abo10164 HIV1-SF2
16	198	100.0	36	8 ADN06923	Adn06923 Peptide #
17	198	100.0	36	8 ADS87258	Ads87258 HIV-1 gp4
18	198	100.0	36	9 ADY17493	Ady17493 HIV-1 tra
19	193	97.5	36	2 AAR67698	Aar67698 DP-178 ho
20	193	97.5	36	2 AAR98399	Aar98399 DP185 cor
21	193	97.5	36	2 AAU17012	Aau17012 DP-178-lik
22	193	97.5	36	3 AAY89836	Aay89836 Core poly
23	193	97.5	36	4 AAG67040	Aag67040 HIV-1 gp4
24	193	97.5	36	4 AAU14012	Aau14012 DP178 hom

25	187	94.4	36	3 AAY89665	Aay89665 Core poly
26	187	94.4	36	4 AAB78086	Aab78086 Core poly
27	187	94.4	36	4 ABB02524	Abb02524 Viral cor
28	187	94.4	36	4 ABB01073	Abb01073 Viral DP1
29	187	94.4	36	4 AAU13619	Aau13619 DP178-lik
30	187	94.4	36	5 ADE02544	Ade02544 Hybrid po
31	187	94.4	48	8 ADU80507	Adu80507 Transmemb
32	187	94.4	48	9 ADZ40285	Adz40285 HIV-1 gp4
33	185	93.4	36	3 AAY89446	Aay89446 Core poly
34	185	93.4	36	3 AAB14575	Aab14575 HIV-1 iso
35	185	93.4	36	4 AAG63902	Aag63902 Amino aci
36	185	93.4	36	4 AAB77847	Aab77847 Core poly
37	185	93.4	36	4 AAU70678	Aau70678 HIV viral
38	185	93.4	36	4 ABB00854	Abb00854 Viral DP1
39	185	93.4	36	4 ABB02329	Abb02329 Viral cor
40	185	93.4	36	4 AAU13400	Aau13400 DP178-lik
41	185	93.4	36	5 ADE02349	Ade02349 Hybrid po
42	185	93.4	36	8 ADN46089	Adn46089 C-helical
43	185	93.4	36	9 ADY29992	Ady29992 HIV-1 gro
44	185	93.4	46	3 AAB14573	Aab14573 HIV-1 iso
45	185	93.4	46	4 AAG63900	Aag63900 Amino aci

ALIGNMENTS

RESULT 1

AAy89837

ID AAY89837 standard; peptide; 36 AA.

XX AAY89837;

AC AAY89837;

XX 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 1406.

XX Retrovirus; hybrid polypeptide; enhancer; gp11; envelope protein; HIV-1;

KW HIV-2; HIV; pharmacokinetic; half-life; growth factor; cytokine; viral;

KW anti-fusogenic; differentiation factor; interleukin; interferon;

KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS Unidentified.

XX WO959615-A1.

PN 25-NOV-1999.

XX 20-MAY-1999; 99WO-US011219.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

DR A new hybrid polypeptide with enhanced pharmacokinetic properties

XX comprises enhancer sequence.

PT Disclosure; Page 45; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp11) protein sequences, especially from HIV-1, HIV-2 and HIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacologically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or angiogenic

Query Match 100.0%; Score 198; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTIYTLLEESQKQKNEQELLELDKWSLWNWF 36
 DB 1 YNTIYTLLEESQKQKNEQELLELDKWSLWNWF 36

RESULT 4
 AAB78238
 ID AAB78238 standard; peptide; 36 AA.
 XX AAB78238;
 AC AAB78238;
 DT 19-APR-2001 (first entry)
 XX Core polypeptide T1406.
 DE
 XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
 KW antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
 KW fusion-related disorder; bacterial infection; viral infection.
 XX Unidentified.
 OS
 XX WO200103723-A1.
 PN
 XX 18-JAN-2001.
 PD
 XX 10-JUL-2000; 2000WO-US018772.
 PF
 XX 09-JUL-1999; 99US-00350641.
 PR
 XX (TRIM-) TRIMERIS INC.
 PA
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 PI WPI; 2001-147136/15.
 DR
 XX New hybrid polypeptide, useful for preventing, treating and diagnosing
 PT e.g. viral infections, comprises an enhancer peptide linked to a core
 PT polypeptide.
 XX Disclosure; Page 58; 151pp; English.
 XX The present sequence is a core polypeptide which may be linked to an
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to
 CC those exhibited by the core polypeptide when introduced into a living
 CC system. It is used to increase the in vitro or ex vivo half-life of the
 CC core polypeptide. The hybrid and core polypeptides can be used for
 CC modulating fusogenic events and intracellular processes involving coiled-
 CC coil peptide interactions. Other uses include preventing, treating and/or
 CC diagnosing disorders involving fusion events (e.g. modulation of
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral
 CC infections caused by human immunodeficiency virus, respiratory syncytial
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
 CC polio virus). The enhancer peptide sequence increases the half-life and
 CC reduces the clearance rate of therapeutic peptides, which increases their
 CC efficacy and minimises the incidence and severity of adverse side
 CC effects. In addition, this increases the sensitivity of the diagnostic
 CC procedure in which they are used
 XX SQ Sequence 36 AA;

Query Match 100.0%; Score 198; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTIYTLLEESQKQKNEQELLELDKWSLWNWF 36

DB 1 YNTIYTLLEESQKQKNEQELLELDKWSLWNWF 36

RESULT 5
 AAB78237
 ID AAB78237 standard; peptide; 36 AA.
 XX AAB78237;
 AC AAB78237;
 DT 19-APR-2001 (first entry)
 XX Core polypeptide T1405.
 DE
 XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
 KW antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
 KW fusion-related disorder; bacterial infection; viral infection.
 XX Unidentified.
 OS
 XX WO200103723-A1.
 PN
 XX 18-JAN-2001.
 PD
 XX 10-JUL-2000; 2000WO-US018772.
 PF
 XX 09-JUL-1999; 99US-00350641.
 PR
 XX (TRIM-) TRIMERIS INC.
 PA
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 PI WPI; 2001-147136/15.
 DR
 XX New hybrid polypeptide, useful for preventing, treating and diagnosing
 PT e.g. viral infections, comprises an enhancer peptide linked to a core
 PT polypeptide.
 XX Disclosure; Page 58; 151pp; English.
 XX The present sequence is a core polypeptide which may be linked to an
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to
 CC those exhibited by the core polypeptide when introduced into a living
 CC system. It is used to increase the in vitro or ex vivo half-life of the
 CC core polypeptide. The hybrid and core polypeptides can be used for
 CC modulating fusogenic events and intracellular processes involving coiled-
 CC coil peptide interactions. Other uses include preventing, treating and/or
 CC diagnosing disorders involving fusion events (e.g. modulation of
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral
 CC infections caused by human immunodeficiency virus, respiratory syncytial
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
 CC polio virus). The enhancer peptide sequence increases the half-life and
 CC reduces the clearance rate of therapeutic peptides, which increases their
 CC efficacy and minimises the incidence and severity of adverse side
 CC effects. In addition, this increases the sensitivity of the diagnostic
 CC procedure in which they are used
 XX SQ Sequence 36 AA;

Query Match 100.0%; Score 198; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTIYTLLEESQKQKNEQELLELDKWSLWNWF 36
 DB 1 YNTIYTLLEESQKQKNEQELLELDKWSLWNWF 36

RESULT 6
 AAU70180

ID AAU70180 standard; peptide; 36 AA.
 AC AAU70180;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE HIV viral envelope protein stabilising peptide #2.
 XX
 DE Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;
 KW anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
 KW alpha-helical region; ectodomain.
 KW
 XX
 OS Homo sapiens.
 XX
 XX WO200170262-A2.
 PN
 XX
 XX 27-SEP-2001.
 PD
 XX
 XX 15-MAR-2001; 2001WO-US008108.
 PF
 XX
 XX 17-MAR-2000; 2000US-0189981P.
 PR
 XX
 XX (PANA-) PANACOS PHARM INC.
 PA
 XX
 XX Wild CT, Allaway GP;
 PI
 XX
 XX WPI; 2001-626098/72.
 DR
 XX
 XX Immunogenic composition for inhibiting HIV infection, comprises viral
 PT envelope protein or its fragment exterior to viral membrane, a
 PT stabilising peptide, and, optionally, viral cell surface receptor or its
 PT fragment.
 PT
 XX
 XX Claim 6; Page 45; 84pp; English.
 PS
 XX
 CC The invention relates to methods of generating immunogens that elicit
 CC neutralising antibodies which target regions of viral envelope proteins
 CC such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-
 CC 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and
 CC AAU70677-AAU70743 represent stabilising peptides modelling the alpha-
 CC helical regions of the ectodomain of the HIV-1 transmembrane protein to
 CC stabilise fusion-active intermediate structures, which can be used as
 CC vaccine immunogens. Immunogenic compositions comprise a viral envelope
 CC protein or its fragment exterior to the viral membrane, a stabilising
 CC peptide to disrupt formation of structural intermediates necessary for
 CC viral fusion and entry, and optionally, a viral cell surface receptor or
 CC its fragment. The stabilising peptide is capable of associating with the
 CC envelope protein or its fragment to form a stabilised, fusion active
 CC structure. Antibody binding assays are used to determine the ability of
 CC immunogen vaccines to generate an immune response to various forms of
 CC envelope. Virus neutralisation assays can be used to characterise the
 CC antibody response raised against HIV-1 gp41 domains. The sequences and
 CC methods are useful for inhibiting HIV infection, for inducing an immune
 CC response in an animal and for raising antibodies
 XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 198; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YNTNTIYTLLEESQNOQKNEQELLELDKWSLWNWF 36
 Db 1 YNTNTIYTLLEESQNOQKNEQELLELDKWSLWNWF 36
 RESULT 7
 ABB02830
 ID ABB02830 standard; peptide; 36 AA.
 XX
 AC ABB02830;
 XX
 DT 11-SEP-2003 (revised)

DT 06-AUG-2003 (revised)
 DT 03-JAN-2002 (first entry)
 XX
 DE Viral core polypeptide, SEQ ID NO: 1357.
 XX
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 KW infection.
 KW
 XX Viruses.
 OS
 XX WO200164013-A2.
 PN
 XX
 XX 07-SEP-2001.
 PD
 XX
 XX 07-FEB-2001; 2001WO-US003988.
 PF
 XX
 XX 29-FEB-2000; 2000US-00515965.
 PR
 XX
 XX (TRIM-) TRIMERIS INC.
 PA
 XX
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
 PI WPI; 2001-514829/56.
 XX
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus
 PT infection.
 PT
 XX
 PS Disclosure; Page 524; 587pp; English.
 CC
 CC The invention relates to isolated analogues of the heptad repeat region
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
 CC regions of proteins interact non-covalently with each other and/or with
 CC peptides derived from them. This interaction is required for normal
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region
 CC peptide analogues may be used to inhibit respiratory syncytial virus
 CC (RSV) infection in a cell. They may also be used to inhibit HIV
 CC infection. The present sequence is a peptide provided in the
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
 CC 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 198; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YNTNTIYTLLEESQNOQKNEQELLELDKWSLWNWF 36
 Db 1 YNTNTIYTLLEESQNOQKNEQELLELDKWSLWNWF 36
 RESULT 8
 ABB01245
 ID ABB01245 standard; peptide; 36 AA.
 XX
 AC ABB01245;
 XX
 DT 11-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 03-JAN-2002 (first entry)
 XX
 DE Viral DP178/107-like region peptide T1406.
 XX
 XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 KW infection.
 KW
 XX Viruses.
 OS

PN WO200164013-A2.
XX
PD 07-SEP-2001.
XX
PF 07-FEB-2001; 2001WO-US003988.
XX
PR 29-FEB-2000; 2000US-00515965.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX
XX WPI; 2001-514829/56.
XX
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
PT fusion, useful for treating HIV and Respiratory Syncytial Virus
PT infection.
XX
XX Disclosure; Page 58; 587pp; English.
XX
XX The invention relates to isolated analogues of the heptad repeat region
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
CC regions of proteins interact non-covalently with each other and/or with
CC peptides derived from them. This interaction is required for normal
CC infectivity of viruses such as RSV and HIV. The heptad repeat region
CC peptide analogues may be used to inhibit respiratory syncytial virus
CC (RSV) infection in a cell. They may also be used to inhibit HIV
CC infection. The present sequence is a peptide provided in the
CC specification. (Updated on 08-AUG-2003 to correct OS field.) (Updated on
CC 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNITVLTLESQNOQEKNEQELLELDKWASLWNWF 36
DB 1 YNTNITVLTLESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 9
ABB01244
ID ABB01244 standard; peptide; 36 AA.
XX
AC ABB01244;
XX
XX 11-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 03-JAN-2002 (first entry)
XX
XX Viral DP178/107-like region peptide T1405.
DE
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
KW infection.
XX
OS Viruses.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "N-terminal is substituted by Ac"
FT Modified-site 36
FT /note= "C-terminal amide"
XX
XX WO200164013-A2.
PN
XX
PD 07-SEP-2001.
XX
XX 07-FEB-2001; 2001WO-US003988.
PF

XX
PR 29-FEB-2000; 2000US-00515965.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX
XX WPI; 2001-514829/56.
XX
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
PT fusion, useful for treating HIV and Respiratory Syncytial Virus
PT infection.
XX
XX Disclosure; Page 58; 587pp; English.
XX
XX The invention relates to isolated analogues of the heptad repeat region
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
CC regions of proteins interact non-covalently with each other and/or with
CC peptides derived from them. This interaction is required for normal
CC infectivity of viruses such as RSV and HIV. The heptad repeat region
CC peptide analogues may be used to inhibit respiratory syncytial virus
CC (RSV) infection in a cell. They may also be used to inhibit HIV
CC infection. The present sequence is a peptide provided in the
CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
CC 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNITVLTLESQNOQEKNEQELLELDKWASLWNWF 36
DB 1 YNTNITVLTLESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 10
AAU13791
ID AAU13791 standard; peptide; 36 AA.
XX
AC AAU13791;
XX
XX 21-NOV-2001 (first entry)
DT
XX DP178-like/DP107-like peptide T-1406.
DE
XX
XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
KW antifusogenic; antiviral; HIV transmission; mutant; mutein.
XX
XX Human immunodeficiency virus 1; isolate LAI.
OS Synthetic.
XX
XX WO200151673-A2.
PN
XX
XX 19-JUL-2001.
PD
XX
XX 05-JUL-2000; 2000WO-US035727.
PF
XX
XX 09-JUL-1999; 99US-00350841.
PR
XX
XX (TRIM-) TRIMERIS INC.
PA
XX
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
PI
XX
XX WPI; 2001-442157/47.
DR
XX
XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.

Query Match 100.0%; Score 198; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36
|||||
DB 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36
|||||

RESULT 13

ADE02850
ID ADE02850 standard; peptide; 36 AA.

XX AC ADE02850;

DT 29-JAN-2004 (first entry)

XX Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1357.

XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;

XX pharmacokinetic; fusogenic; insulin; diabetes.

XX Unidentified.

XX US6348568-B1.

XX 19-FEB-2002.

XX 20-MAY-1999; 99US-00315304.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2002-424396/45.

XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral
PT activity, has enhancer peptide sequence derived from retroviral envelope
PT protein sequences linked to core polypeptide e.g. therapeutic protein.

XX Disclosure; SEQ ID NO 1357; 70pp; English.

XX The invention relates to a novel hybrid polypeptide comprising an
CC enhancer peptide sequence linked to a core polypeptide. The enhancer
CC peptide sequence comprises WOEWQKI or WASLWFW. The invention also
CC includes novel peptides that exhibit anti-fusogenic activity, antiviral
CC activity and/or ability to modulate intracellular processes. The novel
CC hybrid polypeptide has virucide and antidiabetic activity. The enhancer
CC peptide sequence enhances pharmacokinetic properties of any core
CC polypeptide, for example, a polypeptide useful for the treatment or
CC prevention of a disease, or an imaging agent useful for imaging
CC structures in vivo. The core polypeptides and hybrid polypeptides are
CC useful for modulating fusogenic events and exhibit antifusogenic or
CC antiviral activity. The novel hybrid polypeptide is useful for decreasing
CC viral infection and modulating intracellular processes involving coiled-
CC coil peptide interactions. The novel hybrid polypeptide comprises insulin
CC or its fragment, so the core polypeptide is useful for ameliorating the
CC symptoms of forms of diabetes. The novel hybrid polypeptide is also
CC useful as a part of prognosis for preventing disorders including fusion
CC events and viral infection that involves cell-cell and/or virus-cell
CC fusion, and for diagnosis and in vivo imaging methods. This sequence
CC represents an enhancer peptide of the invention.

XX Sequence 36 AA;

Query Match 100.0%; Score 198; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36
|||||

DB 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 14

ADE02716
ID ADE02716 standard; peptide; 36 AA.

XX AC ADE02716;

DT 29-JAN-2004 (first entry)

XX Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1223.

XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;

XX pharmacokinetic; fusogenic; insulin; diabetes.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Residue is modified by acetyl group"

FT Modified-site 36

FT /note= "C-terminal amide"

XX US6348568-B1.

XX 19-FEB-2002.

XX 20-MAY-1999; 99US-00315304.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2002-424396/45.

XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral
PT activity, has enhancer peptide sequence derived from retroviral envelope
PT protein sequences linked to core polypeptide e.g. therapeutic protein.

XX Disclosure; SEQ ID NO 1223; 70pp; English.

XX The invention relates to a novel hybrid polypeptide comprising an
CC enhancer peptide sequence linked to a core polypeptide. The enhancer
CC peptide sequence comprises WOEWQKI or WASLWFW. The invention also
CC includes novel peptides that exhibit anti-fusogenic activity, antiviral
CC activity and/or ability to modulate intracellular processes. The novel
CC hybrid polypeptide has virucide and antidiabetic activity. The enhancer
CC peptide sequence enhances pharmacokinetic properties of any core
CC polypeptide, for example, a polypeptide useful for the treatment or
CC prevention of a disease, or an imaging agent useful for imaging
CC structures in vivo. The core polypeptides and hybrid polypeptides are
CC useful for modulating fusogenic events and exhibit antifusogenic or
CC antiviral activity. The novel hybrid polypeptide is useful for decreasing
CC viral infection and modulating intracellular processes involving coiled-
CC coil peptide interactions. The novel hybrid polypeptide comprises insulin
CC or its fragment, so the core polypeptide is useful for ameliorating the
CC symptoms of forms of diabetes. The novel hybrid polypeptide is also
CC useful as a part of prognosis for preventing disorders including fusion
CC events and viral infection that involves cell-cell and/or virus-cell
CC fusion, and for diagnosis and in vivo imaging methods. This sequence
CC represents an enhancer peptide of the invention.

XX Sequence 36 AA;

Query Match 100.0%; Score 198; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36
|||||

Search completed: March 6, 2006, 15:37:19
Job time : 117.667 secs

Db 1 YNTYITVLTLEESQKQKNEQELLELDKQASLWNWF 36

RESULT 15

ABO10164
ID ABO10164 standard; peptide; 36 AA.

XX AC ABO10164;

XX DT 23-OCT-2003 (revised)

XX DT 19-AUG-2003 (first entry)

XX DE HIV1-SF2 gp41 protein, DP85 peptide.

XX KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;

XX KW Epstein-Barr virus infection; heptad repeat motif.

XX OS Human immunodeficiency virus 1; isolate SF2.

XX PN US6518013-B1.

XX PD 11-FEB-2003.

XX PF 07-JUN-1995; 95US-00485546.

XX PR 07-JUN-1993; 93US-00073028.

XX PR 07-JUN-1994; 94US-00255208.

XX PR 20-DEC-1994; 94US-00360107.

XX PA (TRIM-) TRIMERIS INC.

XX PI Barney SO, Lambert DM, Petteway SR;

XX DR WPI; 2003-465599/44.

PT Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
PT the cell with a peptide consisting of a region of Epstein-Barr virus
PT protein.

PS Example; Fig 1; 716pp; English.

XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective
CC concentration of a peptide consisting of a region of 16-39 consecutive
CC amino acids of an Epstein-Barr virus protein for an effective period of
CC time, where the region is recognised by one or more of ALLMOR15,
CC 107X178x4 or PLZIP sequence search motifs, the peptide further comprises
CC an amino terminal X, and a carboxy terminal Z in which X comprises an
CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
CC group or macromolecular carrier group, and Z comprises a carboxyl group,
CC amido group, hydrophobic group, or macromolecular carrier group, and
CC fusion of the virus to the cell is inhibited. The peptides were
CC identified by analysing the structure/motifs present in the HIV-1
CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
CC motif containing peptides were used to design the motifs cited above,
CC which in turn were used to analyse proteins from other pathogenic
CC organisms and HIV isolates, looking for DP107/178 structural analogues.
CC The method is useful for inhibiting transmission of Epstein-Barr virus to
CC a cell and Epstein-Barr virus infection. The present sequence is a
CC control peptide used in the study of the DP178 structure. (Updated on 23-
CC OCT-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 199; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. No. 3.4e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITVLTLEESQKQKNEQELLELDKQASLWNWF 36

Db 1 YNTYITVLTLEESQKQKNEQELLELDKQASLWNWF 36

DR ENBL; U06729; AAA19142.1; -, mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 .DR Pfam; PF00517; GP41; 1.
 FT NON_TER 1
 FT NON_TER 50
 ST SEQUENCE 50 AA; 6287 MW; EABA093F0877D85B CRC64;
 Query Match 86.4%; Score 173; DB 2; Length 50;
 Best Local Similarity 86.1%; Pred. No. 6.5e-13;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps

Oy 1 YTNVTYTLLESNQOEKNEQELLELDKWASLWNWF 36
 |||||||
 Db 15 YTGVIYTLLESNQOEKNEQELLELDKWANLWNWF 50
 |||||||

RESULT 8
 Q69907_9HIV1 PRELIMINARY; PRT; 49 AA.

AC Q69907;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE GP41 (Fragment).
 GS Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae
 OC Lentivirus; Primate lentivirus group.
 OX NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94211861; PubMed=7512731;
 RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
 KA Keller P.M., Shaw A.R., Emin E.A.;
 RT "Neutralization of divergent human immunodeficiency virus type 1
 RT variants and primary isolates by IAM-41-2P5, an anti-gp41 human
 RT monoclonal antibody.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
 DR ENBL; U06737; AAA19150.1; -, mRNA.
 DR HSPG; Q87973; ZSIV.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_GP41.
 .DR Pfam; PF00517; GP41; 1.
 FT NON_TER 1
 FT NON_TER 49
 ST SEQUENCE 49 AA; 6241 MW; 29C4E5A8CBC7CDD8 CRC64;
 Query Match 86.9%; Score 172; DB 2; Length 49;
 Best Local Similarity 83.3%; Pred. No. 8.5e-13;
 Matches 30; Conservative 4; Mismatches 2; Indels 0; Gaps

Oy 1 YTNVTYTLLESNQOEKNEQELLELDKWASLWNWF 36
 |||||||
 Db 14 YTSLIYTLLESQTQEKEKELLELDKWANLWNWF 49
 |||||||

RESULT 9
 Q69908_9HIV1 PRELIMINARY; PRT; 49 AA.

AC Q69908;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE GP41 (Fragment).
 GS Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae
 OC Lentivirus; Primate lentivirus group.

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OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06738; AAA19151.1; -; mRNA.
DR HSSP; Q87973; 2SIV.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6283 MW; 74CD75339B92C172 CRC64;

Query Match 86.9%; Score 172; DB 2; Length 49;
Best Local Similarity 83.3%; Pred. No. 8.5e-13;
Matches 30; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQKQKNEQELLELDKWASLWNWF 36
|||:|||||:|||||:|||||:|||||:|||||
Db 14 YTSIIYTLLEKSNQKQKNEKELLELDKWTLNWNF 49

RESULT 10
Q69905_9HIV1
ID Q69905_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69905;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06735; AAA19148.1; -; mRNA.
DR HSSP; F31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4196 MW; 7B724A8EA164BD9C CRC64;

Query Match 86.4%; Score 171; DB 2; Length 34;
Best Local Similarity 96.9%; Pred. No. 7.4e-13;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLEESQKQKNEQELLELDKWASLWNWF 36
|||||:|||||:|||||:|||||:|||||
Db 3 IYTLLEKSNQKQKNEQELLELDKWASLWNWF 34

RESULT 11
Q69900_9HIV1
ID Q69900_9HIV1 PRELIMINARY; PRT; 50 AA.
AC Q69900;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06730; AAA19143.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 50
SQ SEQUENCE 50 AA; 6300 MW; EABA093F086C79E1 CRC64;

Query Match 84.8%; Score 168; DB 2; Length 50;
Best Local Similarity 83.3%; Pred. No. 2.6e-12;
Matches 30; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQKQKNEQELLELDKWASLWNWF 36
|||:|||||:|||||:|||||:|||||
Db 15 YTYIYNLLEESQKQKNEQELLELDKWALWNWF 50

RESULT 12
Q69903_9HIV1
ID Q69903_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69903;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06733; AAA19146.1; -; mRNA.
DR HSSP; F31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4226 MW; E609273F6164BD80 CRC64;
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Query Match      84.3%; Score 167; DB 2; Length 34;
Best Local Similarity 93.8%; Pred. No. 2.2e-12;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLESQOQKNEQELLELDKWSLWNWF 36
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Db 3 IYTLLESQOQKNEQELLELDKWSLWNWF 34

RESULT 13
Q69893_9HIV1
ID Q69893_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69893;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2P5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06723; AAA19136.1; -; mRNA.
DR HSSP; P31872; ILBO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 34
FT NON TER 34 34
SQ SEQUENCE 34 AA; 4196 MW; 0C7CAA60A164B89C CRC64;

Query Match      83.8%; Score 166; DB 2; Length 34;
Best Local Similarity 96.9%; Pred. No. 2.9e-12;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IYTLLESQOQKNEQELLELDKWSLWNWF 36
   |||||:|||||:|||||:|||||:|||||
Db 3 IYTLLESQOQKNEQELLELDKWSLWNWF 34

RESULT 14
Q69894_9HIV1
ID Q69894_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69894;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2P5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
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DR EMBL; U06724; AAA19137.1; -; mRNA.
DR HSSP; P31872; ILBO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 34
FT NON TER 34 34
SQ SEQUENCE 34 AA; 4182 MW; A37CAA60A164AEF0 CRC64;

Query Match      83.8%; Score 166; DB 2; Length 34;
Best Local Similarity 96.9%; Pred. No. 2.9e-12;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IYTLLESQOQKNEQELLELDKWSLWNWF 36
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Db 3 IYTLLESQOQKNEQELLELDKWSLWNWF 34

RESULT 15
Q69904_9HIV1
ID Q69904_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69904;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2P5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06734; AAA19147.1; -; mRNA.
DR HSSP; P31872; ILBO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 34
FT NON TER 34 34
SQ SEQUENCE 34 AA; 4184 MW; BB1CAA65F131AD5A CRC64;

Query Match      82.3%; Score 163; DB 2; Length 34;
Best Local Similarity 90.6%; Pred. No. 6.5e-12;
Matches 29; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 IYTLLESQOQKNEQELLELDKWSLWNWF 36
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Db 3 IYTLLESQOQKNEQELLELDKWSLWNWF 34

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OM protein - protein search, using sw model

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(without alignments)
107.578 Million cell updates/sec

Title: US-09-809-060A-2
Perfect score: 198
Sequence: 1 YNTIYTLLESQNKQKNEQELLELDKWLWNP 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	36	2 US-08-486-099-3	Sequence 3, Appli
2	198	100.0	36	2 US-08-484-223B-3	Sequence 3, Appli
3	198	100.0	36	2 US-08-919-597-3	Sequence 3, Appli
4	198	100.0	36	2 US-08-475-668A-3	Sequence 3, Appli
5	198	100.0	36	2 US-08-485-551A-3	Sequence 3, Appli
6	198	100.0	36	2 US-08-471-913A-3	Sequence 3, Appli
7	198	100.0	36	2 US-08-485-264A-3	Sequence 3, Appli
8	198	100.0	36	2 US-09-082-279B-1357	Sequence 1357, Ap
9	198	100.0	36	2 US-08-474-349A-3	Sequence 3, Appli
10	198	100.0	36	2 US-09-315-304B-1357	Sequence 1357, Ap
11	198	100.0	36	2 US-08-255-208A-3	Sequence 3, Appli
12	198	100.0	36	2 US-08-973-952-3	Sequence 3, Appli
13	198	100.0	36	2 US-08-470-896-3	Sequence 3, Appli
14	198	100.0	36	2 US-08-485-546A-3	Sequence 3, Appli
15	198	100.0	36	2 US-09-834-784-1357	Sequence 1357, Ap
16	198	100.0	36	2 US-09-515-965A-1357	Sequence 1357, Ap
17	198	100.0	36	2 US-09-350-641C-1357	Sequence 1357, Ap
18	198	100.0	36	2 US-09-350-841A-1357	Sequence 1357, Ap
19	198	100.0	36	2 US-08-487-266A-3	Sequence 3, Appli
20	198	100.0	36	2 US-09-623-548A-1421	Sequence 1421, Ap
21	198	100.0	36	2 US-10-252-136-3	Sequence 3, Appli
22	198	100.0	36	2 US-09-657-276-1421	Sequence 1421, Ap
23	198	100.0	36	2 US-08-484-741-3	Sequence 3, Appli
24	193	97.5	36	1 US-08-073-028-3	Sequence 3, Appli
25	193	97.5	36	2 US-08-360-107A-3	Sequence 3, Appli
26	193	97.5	36	2 US-08-554-616-3	Sequence 3, Appli
27	193	97.5	36	2 US-09-350-841A-1543	Sequence 1543, Ap

Query Match 100.0%; Score 198; DB 2; Length 36;

28 187 94.4 36 2 US-09-082-279B-1051 Sequence 1051, Ap
29 187 94.4 36 2 US-09-315-304B-1051 Sequence 1051, Ap
30 187 94.4 36 2 US-09-834-784-1051 Sequence 1051, Ap
31 187 94.4 36 2 US-09-515-965A-1051 Sequence 1051, Ap
32 187 94.4 36 2 US-09-350-641C-1051 Sequence 1051, Ap
33 187 94.4 36 2 US-09-350-841A-1051 Sequence 1051, Ap
34 185 93.4 36 2 US-09-082-279B-856 Sequence 856, App
35 185 93.4 36 2 US-09-315-304B-856 Sequence 856, App
36 185 93.4 36 2 US-09-834-784-856 Sequence 856, App
37 185 93.4 36 2 US-09-779-451-47 Sequence 47, Appl
38 185 93.4 36 2 US-09-515-965A-856 Sequence 856, App
39 185 93.4 36 2 US-09-350-641C-856 Sequence 856, App
40 185 93.4 36 2 US-09-350-841A-856 Sequence 856, App
41 185 93.4 46 2 US-09-779-451-45 Sequence 109, Appl
42 183 92.4 46 2 US-08-965-056-109 Sequence 409, Appl
43 181 91.4 36 2 US-09-082-279B-642 Sequence 642, App
44 181 91.4 36 2 US-09-315-304B-642 Sequence 642, App
45 181 91.4 36 2 US-09-834-784-642 Sequence 642, App

ALIGNMENTS

RESULT 1

US-08-486-099-3
; Sequence 3, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-486-099-3

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Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLESQKQKNEQELLELDKWASLWNWF 36

RESULT 2
US-08-484-223B-3
; Sequence 3, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonsse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-484-223B-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLESQKQKNEQELLELDKWASLWNWF 36

RESULT 3
US-08-919-597-3
; Sequence 3, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
```

```
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonsse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-919-597-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLESQKQKNEQELLELDKWASLWNWF 36

RESULT 4
US-08-475-668A-3
; Sequence 3, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
```


COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36
|||||
DB 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36

RESULT 5
US-08-485-551A-3
Sequence 3, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36
|||||
DB 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36

RESULT 6
US-08-471-913A-3
Sequence 3, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 7
US-08-485-264A-3
; Sequence 3, Application US/08485264A
; Patent No. 622893
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-485-264A-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 8
US-09-082-279B-1357
; Sequence 1357, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Marutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1357
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-1357

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 9
US-08-474-349A-3
; Sequence 3, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWVNF 36
|||||
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWVNF 36

RESULT 10

US-09-315-304B-1357
; Sequence 1357, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1357
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1357

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWVNF 36
|||||
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWVNF 36

RESULT 11

US-08-255-208A-3
; Sequence 3, Application US/08255208A
; Patent No. 6440656
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway Jr., Stephen R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,208A

; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-255-208A-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWVNF 36
|||||
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWVNF 36

RESULT 12

US-08-973-952-3
; Sequence 3, Application US/08973952A
; Patent No. 6475491
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/08/973,952A
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 08/481,957
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-08-973-952-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWVNF 36
|||||
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWVNF 36

RESULT 13

US-08-470-896-3
; Sequence 3, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION

/ NUMBER OF SEQUENCES: 273
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/470,896
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-020
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-08-470-896-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKNEQKNEQLLELDKWSLWNNWF 36
|||||
Db 1 YNTIYTLLESQKNEQKNEQLLELDKWSLWNNWF 36

RESULT 14
US-08-485-546A-3
Sequence 3, Application US/08485546A
Patent No. 6518013
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A

/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-028
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-08-485-546A-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKNEQKNEQLLELDKWSLWNNWF 36
|||||
Db 1 YNTIYTLLESQKNEQKNEQLLELDKWSLWNNWF 36

RESULT 15
US-09-834-784-1357
Sequence 1357, Application US/09834784
Patent No. 6562787
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1357
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-1357

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKNEQKNEQLLELDKWSLWNNWF 36
|||||
Db 1 YNTIYTLLESQKNEQKNEQLLELDKWSLWNNWF 36

Search completed: March 6, 2006, 15:45:44
Job time : 28.6667 secs

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:31:26 ; Search time 114.667 Seconds
(without alignments)
137.945 Million cell updates/sec

Title: US-09-809-060A-3

Perfect score: 200

Sequence: 1 YTGIIYNLEESQKQKNEQELLELDKWNLWNVF 36

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*

1: Geneseq1990s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003s.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	100.0	36	2 AAR67699	Aar67699 DP-178 ho
2	200	100.0	36	2 AAR98400	Aar98400 Peptide c
3	200	100.0	36	2 AAW17013	Aaw17013 DP-178-li
4	200	100.0	36	4 AAB54787	Aab54787 HIV antiv
5	200	100.0	36	4 AAB92246	Aab92246 Virus rel
6	200	100.0	36	4 AAB78239	Aab78239 Core poly
7	200	100.0	36	4 AAB78240	Aab78240 Core poly
8	200	100.0	36	4 AAU70181	Aau70181 HIV viral
9	200	100.0	36	4 ABB02832	Abb02832 Viral cor
10	200	100.0	36	4 ABB02831	Abb02831 Viral cor
11	200	100.0	36	4 AAG67041	Aag67041 HIV-1 gp4
12	200	100.0	36	4 ABB01246	Abb01246 Viral DP1
13	200	100.0	36	4 ABB01247	Abb01247 Viral DP1
14	200	100.0	36	4 AAU13793	Aau13793 DP178-lik
15	200	100.0	36	4 AAU13792	Aau13792 DP178-lik
16	200	100.0	36	4 AAU14013	Aau14013 DP178 hom
17	200	100.0	36	5 AAO18773	Aao18773 HIV gp41
18	200	100.0	36	5 ADE02851	Ade02851 Hybrid po
19	200	100.0	36	5 ADE02852	Ade02852 Hybrid po
20	200	100.0	36	6 ABO10165	Abo10165 HIV1-RF g
21	200	100.0	36	8 ADN06924	Adn06924 Peptide #
22	200	100.0	36	8 ADS87259	Ads87259 HIV-1 gp4
23	200	100.0	36	9 ADY71494	Ady71494 HIV-1 tra
24	185	92.5	48	8 ADU80528	Adu80528 Transmemb

25	185	92.5	48	9 ADZ40286	Adz40286 HIV-1 gp4
26	184	92.0	36	2 AAR67698	Aar67698 DP-178 ho
27	184	92.0	36	2 AAR98399	Aar98399 DP185 cor
28	184	92.0	36	2 AAW17012	Aaw17012 DP-178-li
29	184	92.0	36	4 AAG67040	Aag67040 HIV-1 gp4
30	184	92.0	36	4 AAU14012	Aau14012 DP178 hom
31	182	91.0	46	2 AAY22914	Aay22914 SEQ ID NO
32	182	91.0	46	5 AAG68385	Ag68385 HIV envel
33	182	91.0	46	6 ABUS7792	Abus7792 Human imm
34	182	91.0	48	8 ADU80508	Adu80508 Transmemb
35	182	91.0	48	8 ADU80513	Adu80513 Transmemb
36	182	91.0	48	8 ADU80527	Adu80527 Transmemb
37	182	91.0	48	9 ADZ40266	Adz40266 HIV-1 gp4
38	182	91.0	48	9 ADZ40271	Adz40271 HIV-1 gp4
39	182	91.0	48	9 ADZ40285	Adz40285 HIV-1 gp4
40	181	90.5	48	8 ADU80507	Adu80507 Transmemb
41	181	90.5	48	9 ADZ40265	Adz40265 HIV-1 gp4
42	180.5	90.2	35	3 AAY89838	Aay89838 Core poly
43	180.5	90.2	35	3 AAY89839	Aay89839 Core poly
44	180	90.0	36	4 AAB77633	Aab77633 Core poly
45	180	90.0	36	4 ABB02115	Abb02115 Viral cor

ALIGNMENTS

RESULT 1

AAR67699

ID AAR67699 standard; peptide; 36 AA.

XX AAR67699;

AC AAR67699;

XX

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 24-AUG-1995 (first entry)

XX

DE DP-178 homologue derived from HIV-1 RP has antiviral activity.

XX

KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;

KW human immunodeficiency virus; transmembrane protein; gp41; alpha helix;

KW leucine zipper; DP-185.

XX

OS Human immunodeficiency virus; (RP isolate).

XX

PN WO9428920-A1.

XX

PD 22-DEC-1994.

XX

PF 07-JUN-1994; 94WO-US005739.

XX

PR 07-JUN-1993; 93US-00073028.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Bolognesi DP, Matthews TJ, Wild CT, Barney SO, Lambert DM;

PI Petteway SR;

XX

DR WPI; 1995-036105/05.

XX

PT Computer search generated synthetic peptides - are inhibitors of HIV

PT transmission.

XX

PS Example; Fig 1; 182pp; English.

XX

CC This peptide is isolated from HIV-1 isolate RP, and is a homologue of the
peptide DP-178. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
isolate LAI transmembrane protein gp41. It forms a putative alpha helix
at the C-terminal end of the gp41 ectodomain, and complexes with DP-107
(corresponds to amino acids 558-595) which contains a leucine zipper
motif. The peptides complex via non-covalent protein-protein
interactions, and possess anti-viral activity. The peptide inhibits
transmission to uninfected cells, and can also be used as type and/or
subtype specific diagnostic tools. (Updated on 25-MAR-2003 to correct PN

CC field.) (Updated on 16-OCT-2003 to standardise OS field)
 XX Sequence 36 AA;

Query Match 100.0%; Score 200; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36
 |||||
 Db 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36

RESULT 2

AAR98400
 ID AAR98400 standard; peptide; 36 AA.

XX AAR98400;

AC AAR98400;

DT 16-OCT-2003 (revised)

DT 17-FEB-1997 (first entry)

XX Peptide corresponding to residues 638-673 of HIV-1(RF) gp41.

XX Antifusogenic activity; antiviral capability; coiled-coil peptide;
 KW ALLMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;
 KW Influenza virus; hepatitis B virus.

XX Human immunodeficiency virus 1.

XX WO9619495-A1.

PN 27-JUN-1996.

XX 20-DEC-1995; 95WO-US016733.

PR 20-DEC-1994; 94US-00360107.

XX 06-JUN-1995; 95US-00470896.

PA (UYDU-) UNIV DUKE

PA (TRIM-) TRIMERIS INC.

XX Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;
 PI Petteway SR, Langlois AJ;

DR WPI; 1996-309517/31.

XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
 PT isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP sequence
 PT search motif.

XX Disclosure; Fig 1; 471pp; English.

XX The sequences given in AAR98398-408 represent peptides which exhibit
 CC antifusogenic activity, antiviral capability and/or the ability to
 CC modulate intracellular processes involving coiled-coil peptide
 CC structures. These peptides are recognised by the ALLMOT15, 107x178x4 and
 CC PLZIP search motifs. These peptides may be used to inhibit the
 CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
 CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 200; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36
 |||||
 Db 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36

RESULT 3

AAW17013
 ID AAW17013 standard; peptide; 36 AA.

XX AAW17013;

AC AAW17013;

DT 17-OCT-2003 (revised)

DT 01-JUL-1997 (first entry)

XX DP-178-like peptide useful for treatment of HIV infection.

XX HIV; SIV; human; simian immunodeficiency virus; glycoprotein 41;
 KW transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;
 KW replication; transmission.

XX Human immunodeficiency virus 1; RF isolate.

XX WO9640191-A1.

PN 19-DEC-1996.

XX 06-JUN-1996; 96WO-US009499.

XX 07-JUN-1995; 95US-00481957.

XX (TRIM-) TRIMERIS INC.

XX Johnson RM, Lambert DM;

XX WPI; 1997-099886/09.

XX Compens. contg. DP-178 or DP-107 in combination with other therapeutic
 PT agent - useful for treatment of HIV infection, esp. by inhibiting
 PT replication or transmission of HIV.

XX Disclosure; Fig 1; 84pp; English.

XX AAW17012-W17016 are DP-178 homologues that are useful in the treatment of
 CC HIV infection. DP-178 is a peptide corresponding to residues 638-673 of
 CC HIV type 1 glycoprotein 41 (gp41) transmembrane protein. DP-178 and its
 CC derivatives/homologues are used in combination with a therapeutic agent,
 CC e.g. a reverse transcriptase, viral protease, cytokine, glycosylation or
 CC viral mRNA processing inhibitor or a nucleoside inhibitor. The peptides
 CC work by inhibiting viral replication or inhibiting transmission. They may
 CC also be used in vaccines for protecting against HIV infection. (Updated
 CC on 17-OCT-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 200; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36
 |||||
 Db 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36

RESULT 4

AAB54787

ID AAB54787 standard; peptide; 36 AA.

XX AAB54787;

AC AAB54787;

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

XX HIV antiviral activity exhibiting peptide SEQ ID NO:4.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;
 KW antifusogenic; mobile blood component; measles virus; MeV; SIV;
 KW simian immunodeficiency virus; human parainfluenza virus; HPiV; RSV;
 KW human respiratory syncytial virus; human immunodeficiency virus; HIV.

OS Human immunodeficiency virus 1.
 XX
 XX WO200069902-A1.
 XX
 XX
 PD 23-NOV-2000.
 XX
 XX
 XX 17-MAY-2000; 2000WO-US013651.
 PF
 XX
 XX 17-MAY-1999; 99US-0134406P.
 PR
 PR 10-SEP-1999; 99US-0153406P.
 XX
 XX (CONJ-) CONJUCHEM INC.
 PA
 XX
 XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
 PI
 XX WPI; 2001-007496/01.
 DR
 XX
 XX A modified peptide and a reactive group which is reactive with amino
 PT groups, hydroxyl groups, or thiol groups on blood components to form
 PT stable covalent bonds useful for treatment of viral infections, e.g.
 PT human immunodeficiency virus.
 XX
 XX Claim 6; Page 173-174; 21pp; English.
 PS
 XX The present invention describes a modified anti-viral peptide (I)
 CC comprising a peptide that exhibits anti-viral activity and a reactive
 CC group which is reactive with amino groups, hydroxyl groups, or thiol
 CC groups on blood components to form stable covalent bonds. (I) has anti-
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce
 CC the level of membrane fusion events between two or more entities, e.g.,
 CC virus-cell or cell-cell, relative to the level of membrane fusion that
 CC occurs in the absence of the peptide. (I) is useful in the treatment of
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
 CC MeV, and SIV. (I) may be administered prophylactically to previously
 CC uninfected individuals. This is useful in cases where an individual has
 CC been subjected to a high risk of exposure to a virus. By bonding of long-
 CC lived components of the blood, such as immunoglobulin, serum albumin, red
 CC blood cells and platelets the activity is extended for days to weeks.
 CC This is due to improved stability in vivo and a reduced susceptibility to
 CC peptidase or protease degradation. This minimises the need for more
 CC frequent, or even continual, administration of the peptides. AAB54784 to
 CC AAB55431 represent peptides used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 XX
 XX Sequence 36 AA;
 SQ
 Query Match 100.0%; Score 200; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTGIIYNLLSESONQEKNEQELLELDKWLNNWF 36
 |||||
 DB 1 YTGIIYNLLSESONQEKNEQELLELDKWLNNWF 36
 |||||
 RESULT 5
 AAB92246
 ID AAB92246 standard; peptide; 36 AA.
 XX
 XX AAB92246;
 AC
 XX
 XX
 DT 22-JUN-2001 (first entry)
 XX
 XX Virus related peptide SEQ ID NO:1422.
 DE
 XX
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyI, maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX

XX (TRIM-) TRIMERIS INC.
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 XX WPI; 2001-147136/15.
 XX
 XX New hybrid polypeptide, useful for preventing, treating and diagnosing
 XX e.g. viral infections, comprises an enhancer peptide linked to a core
 XX polypeptide.
 XX
 XX Disclosure; Page 58; 151pp; English.
 XX
 XX The present sequence is a core polypeptide which may be linked to an
 XX enhancer peptide to form a novel hybrid polypeptide. The hybrid
 XX polypeptide exhibits enhanced pharmacokinetic properties relative to
 XX those exhibited by the core polypeptide when introduced into a living
 XX system. It is used to increase the in vitro or ex vivo half-life of the
 XX core polypeptide. The hybrid and core polypeptides can be used for
 XX modulating fusogenic events and intracellular processes involving coiled-
 XX coil peptide interactions. Other uses include preventing, treating and/or
 XX diagnosing disorders involving fusion events (e.g. modulation of
 XX neurotransmitter exchange and sperm-egg fusion), intracellular processes
 XX involving coiled-coil peptides (e.g. bacterial infections) and viral
 XX infections that involve cell-cell and/or virus-cell fusion (e.g. viral
 XX infections caused by human immunodeficiency virus, respiratory syncytial
 XX virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
 XX polio virus). The enhancer peptide sequence increases the half-life and
 XX reduces the clearance rate of therapeutic peptides, which increases their
 XX efficacy and minimises the incidence and severity of adverse side
 XX effects. In addition, this increases the sensitivity of the diagnostic
 XX procedure in which they are used
 XX
 XX Sequence 36 AA;
 XX
 XX Query Match 100.0%; Score 200; DB 4; Length 36;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36
 XX |||||
 XX Db 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36
 XX |||||
 XX
 XX RESULT 7
 XX AAB78240
 XX ID AAB78240 standard; peptide; 36 AA.
 XX AC AAB78240;
 XX DT 19-APR-2001 (first entry)
 XX DE Core polypeptide T1408.
 XX KW Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
 XX antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
 XX fusion-related disorder; bacterial infection; viral infection.
 XX OS Unidentified.
 XX PN WO200103723-A1.
 XX PD 18-JAN-2001.
 XX PF 10-JUL-2000; 2000WO-US018772.
 XX PR 09-JUL-1999; 99US-00350641.
 XX (TRIM-) TRIMERIS INC.
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 XX WPI; 2001-147136/15.

XX New hybrid polypeptide, useful for preventing, treating and diagnosing
 XX e.g. viral infections, comprises an enhancer peptide linked to a core
 XX polypeptide.
 XX
 XX Disclosure; Page 58; 151pp; English.
 XX
 XX The present sequence is a core polypeptide which may be linked to an
 XX enhancer peptide to form a novel hybrid polypeptide. The hybrid
 XX polypeptide exhibits enhanced pharmacokinetic properties relative to
 XX those exhibited by the core polypeptide when introduced into a living
 XX system. It is used to increase the in vitro or ex vivo half-life of the
 XX core polypeptide. The hybrid and core polypeptides can be used for
 XX modulating fusogenic events and intracellular processes involving coiled-
 XX coil peptide interactions. Other uses include preventing, treating and/or
 XX diagnosing disorders involving fusion events (e.g. modulation of
 XX neurotransmitter exchange and sperm-egg fusion), intracellular processes
 XX involving coiled-coil peptides (e.g. bacterial infections) and viral
 XX infections that involve cell-cell and/or virus-cell fusion (e.g. viral
 XX infections caused by human immunodeficiency virus, respiratory syncytial
 XX virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
 XX polio virus). The enhancer peptide sequence increases the half-life and
 XX reduces the clearance rate of therapeutic peptides, which increases their
 XX efficacy and minimises the incidence and severity of adverse side
 XX effects. In addition, this increases the sensitivity of the diagnostic
 XX procedure in which they are used
 XX
 XX Sequence 36 AA;
 XX
 XX Query Match 100.0%; Score 200; DB 4; Length 36;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36
 XX |||||
 XX Db 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36
 XX |||||
 XX
 XX RESULT 8
 XX AAU70181
 XX ID AAU70181 standard; peptide; 36 AA.
 XX AC AAU70181;
 XX DT 14-FEB-2002 (first entry)
 XX DE HIV viral envelope protein stabilising peptide #3.
 XX KW Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;
 XX anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
 XX alpha-helical region; ectodomain.
 XX OS Homo sapiens.
 XX PN WO200170262-A2.
 XX PD 27-SEP-2001.
 XX PF 15-MAR-2001; 2001WO-US008108.
 XX PR 17-MAR-2000; 2000US-0189981P.
 XX (PANA-) PANACOS PHARM INC.
 XX Wild CT, Allaway GP;
 XX WPI; 2001-626098/72.
 XX
 XX Immunogenic composition for inhibiting HIV infection, comprises viral
 XX envelope protein or its fragment exterior to viral membrane, a
 XX stabilizing peptide, and, optionally, viral cell surface receptor or its
 XX fragment.

PS Claim 6; Page 45; 84pp; English.

XX The invention relates to methods of generating immunogens that elicit
 CC neutralising antibodies which target regions of viral envelope proteins
 CC such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-
 CC 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and
 CC AAU70677-AAU70743 represent stabilising peptides modelling the alpha-
 CC helical regions of the ectodomain of the HIV-1 transmembrane protein to
 CC stabilise fusion-active intermediate structures, which can be used as
 CC vaccine immunogens. Immunogenic compositions comprise a viral envelope
 CC protein or its fragment exterior to the viral membrane, a stabilising
 CC peptide to disrupt formation of structural intermediates necessary for
 CC viral fusion and entry, and optionally, a viral cell surface receptor or
 CC its fragment. The stabilising peptide is capable of associating with the
 CC envelope protein or its fragment to form a stabilised, fusion active
 CC structure. Antibody binding assays are used to determine the ability of
 CC immunogen vaccines to generate an immune response to various forms of
 CC envelope. Virus neutralisation assays can be used to characterise the
 CC antibody response raised against HIV-1 gp41 domains. The sequences and
 CC methods are useful for inhibiting HIV infection, for inducing an immune
 CC response in an animal and for raising antibodies

SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESNQOEKNEQELLELDKQANLWNWF 36
 |||||
 DB 1 YTGIIYNLLEESNQOEKNEQELLELDKQANLWNWF 36

RESULT 9

ABB02832
 ID ABB02832 standard; peptide; 36 AA.

XX ABB02832;

XX 11-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 03-JAN-2002 (first entry)

XX Viral core polypeptide, SEQ ID NO: 1359.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 KW infection.

XX Viruses.

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US003988.

XX 29-FEB-2000; 2000US-00515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus
 PT infection.

XX Disclosure; Page 525; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-

CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
 CC regions of proteins interact non-covalently with each other and/or with
 CC peptides derived from them. This interaction is required for normal
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region
 CC peptide analogues may be used to inhibit respiratory syncytial virus
 CC (RSV) infection in a cell. They may also be used to inhibit HIV
 CC infection. The present sequence is a peptide provided in the
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
 CC 11-SEP-2003 to standardise OS field)

XX SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESNQOEKNEQELLELDKQANLWNWF 36
 |||||
 DB 1 YTGIIYNLLEESNQOEKNEQELLELDKQANLWNWF 36

RESULT 10

ABB02831
 ID ABB02831 standard; peptide; 36 AA.

XX ABB02831;

XX 11-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 03-JAN-2002 (first entry)

XX Viral core polypeptide, SEQ ID NO: 1358.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 KW infection.

XX Viruses.

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US003988.

XX 29-FEB-2000; 2000US-00515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus
 PT infection.

XX Disclosure; Page 524-525; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
 CC regions of proteins interact non-covalently with each other and/or with
 CC peptides derived from them. This interaction is required for normal
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region
 CC peptide analogues may be used to inhibit respiratory syncytial virus
 CC (RSV) infection in a cell. They may also be used to inhibit HIV
 CC infection. The present sequence is a peptide provided in the
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
 CC 11-SEP-2003 to standardise OS field)

SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36
 |||||
 DB 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36
 |||||

RESULT 11

AAG67041
 ID AAG67041 standard; peptide; 36 AA.

XX AAG67041;

XX 11-SEP-2003 (revised)

DT 03-JAN-2002 (first entry)

XX HIV-1 gp41 peptide DP178 homologue DP-185.

XX Human immunodeficiency virus 1.
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 KW infection; DP185.

XX Human immunodeficiency virus 1.

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US003988.

XX 29-FEB-2000; 2000US-00515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus
 PT infection.

XX Example; Fig 1; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
 CC regions of proteins interact non-covalently with each other and/or with
 CC peptides derived from them. This interaction is required for normal
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region
 CC peptide analogues may be used to inhibit respiratory syncytial virus
 CC (RSV) infection in a cell. They may also be used to inhibit HIV
 CC infection. The present sequence is a peptide provided in the
 CC specification. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36
 |||||
 DB 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36
 |||||

RESULT 12

ABB01246

ID ABB01246 standard; peptide; 36 AA.

XX ABB01246;

XX 11-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 03-JAN-2002 (first entry)

XX Viral DP178/107-like region peptide T1407.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
 KW infection.

XX Viruses.

XX Key Location/Qualifiers

FH Modified-site 1

FT /note= "N-terminal is substituted by Ac"

FT Modified-site 36

FT /note= "C-terminal amide"

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US003988.

XX 29-FEB-2000; 2000US-00515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus
 PT infection.

XX Disclosure; Page 58; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
 CC regions of proteins interact non-covalently with each other and/or with
 CC peptides derived from them. This interaction is required for normal
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region
 CC peptide analogues may be used to inhibit respiratory syncytial virus
 CC (RSV) infection in a cell. They may also be used to inhibit HIV
 CC infection. The present sequence is a peptide provided in the
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
 CC 11-SEP-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 200; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36
 |||||
 DB 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36
 |||||

RESULT 13

ABB01247

ID ABB01247 standard; peptide; 36 AA.

XX ABB01247;

XX 11-SEP-2003 (revised)

PP	05-JUL-2000; 2000WO-US035727.	
XX		
PR	09-JUL-1999; 99US-00350841.	
XX		
PA	(TRIM-) TRIMERIS INC.	
XX		
PI	Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;	
XX	WPI; 2001-442157/47.	
XX		
PT	Identifying a compound that inhibits the formation of or disrupts a	
PT	DP107/DP178 complex, especially compounds with antifuogenic, antiviral	
PT	or intracellular modulatory activity, by detecting the formation of a	
PT	DP107/DP178 complex.	
XX		
XX	Disclosure; Page 77; 259pp; English.	
PS		
XX		
CC	The present invention relates to peptides which exhibit anti-retroviral	
CC	activity. The peptides of the invention (AAU12559-AAU14009) comprise	
CC	DP178-like and DP107-like peptides. The DP178 peptide corresponds to	
CC	amino acids 639-673 of the transmembrane protein gp41 from human	
CC	immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide	
CC	corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention	
CC	also relates to a method of identifying compounds that inhibit the	
CC	formation of or disrupts a DP107/DP178 complex. The method comprises	
CC	detecting the formation of a DP107/DP178 complex, both in the presence or	
CC	absence of a test compound, in a reaction mixture containing DP107 and	
CC	DP178 peptides. The method is useful for identifying compounds, including	
CC	small molecule compounds, which may themselves exhibit antifusogenic,	
CC	antiviral or intracellular modulatory activity. The DP178-like/DP107-like	
CC	peptides are useful to inhibit human and non-human retroviral,	
CC	particularly HIV, transmission to uninfected cells. The present sequence	
CC	represents one of the DP178-like/DP107-like peptides of the invention	
XX		
XX	Sequence 36 AA;	

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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:37:45 ; Search time 18.3333 Seconds
(without alignments)
188.935 Million cell updates/sec

Title: US-09-809-060A-3
Perfect score: 200
Sequence: 1 YTGIIYNLLESONQKNEQELLELDKWNANLWNP 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	21.0	36	2 D83682	hypothetical prote
2	41	20.5	24	2 S01808	hemoglobin AII - t
3	41	20.5	45	2 S01814	hemoglobin BII - t
4	39	19.5	50	2 D83972	hypothetical prote
5	39	19.5	50	2 F86472	5.7K hypothetical
6	38	19.0	43	2 S02031	zinc-binding prote
7	37	18.5	42	2 I48240	LDH-A - mouse (fra
8	37	18.5	44	2 S53113	GUT8-2a protein -
9	36.5	18.2	40	2 S77793	transketolase (EC
10	36	18.0	32	2 I45523	tropomycin T 4f - ra
11	36	18.0	38	2 I66797	tropomycin T 3f - ra
12	36	18.0	41	2 T48342	hypothetical prote
13	36	18.0	48	2 S74261	tropomycin T3f, fast
14	36	18.0	49	2 T05923	high light-inducib
15	35	17.5	30	2 I77411	renin-2 - mouse (f
16	35	17.5	30	2 A34461	heat shock protein
17	35	17.5	50	2 T05541	probable NADPH-fer
18	34.5	17.2	45	2 T52125	R2R3-MYB transcrip
19	34	17.0	49	2 AG3362	hypothetical prote
20	34	17.0	50	2 PU0026	photosystem I 9K p
21	33.5	16.8	43	2 D83894	hypothetical prote
22	33	16.5	33	2 A82186	hypothetical prote
23	33	16.5	38	2 C97551	gene 60 protein -
24	33	16.5	47	2 S31005	pachytene arrest p
25	33	16.5	50	2 S72456	hypothetical prote
26	32.5	16.2	41	2 D71345	homeotic protein H
27	32.5	16.2	46	2 B3474	L33 protein (impor
28	32.5	16.2	49	2 E97287	calreticulin, uter
29	32	16.0	29	2 E33208	

30 32 16.0 30 2 H70152
31 32 16.0 35 2 S71915
32 32 16.0 38 2 H82256
33 32 16.0 39 2 C95128
34 32 16.0 41 2 I65645
35 32 16.0 42 2 T07291
36 32 16.0 43 2 T07503
37 32 16.0 44 2 C34327
38 32 16.0 48 2 S61472
39 32 16.0 48 2 F85646
40 32 16.0 49 2 B48396
41 32 16.0 50 2 AF0140
42 31.5 15.8 48 2 G89944
43 31 15.5 31 2 H82533
44 31 15.5 33 2 S23321
45 31 15.5 35 2 D95229

ALIGNMENTS

RESULT 1

D83682
hypothetical protein BH0260 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: D83682

R:Takami, H.; Nakaseone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran

Nucleic Acids Res. 28, 4317-4331, 2000

A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and s

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: D83682

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-36 <STO>

A:Cross-references: UNIPROT:Q9KGS3; UNIPARC:UPI0000139521; GB:AP001507; GB:BA000004; NID:

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH0260

Query Match 21.0%; Score 42; DB 2; Length 36;

Best Local Similarity 47.6%; Pred. No. 1.2e+02;

Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 8 LLESONQKNEQELLELDK 28

Db 4 LVNESWEQQRKKIQQLSDEX 24

RESULT 2

S01808

hemoglobin AII - tube worm (Lamellibrachia sp.) (fragment)

C:Species: Lamellibrachia sp.

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: S01808

R:Suzuki, T.; Takagi, T.; Ohta, S.

Biochem. J. 255, 541-545, 1988

A>Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably

A:Reference number: S01807; MUID:89076216; PMID:3202832

A:Accession: S01808

A:Molecule type: protein

A:Residues: 1-24 <SUZ>

A:Cross-references: UNIPROT:Q9TWS6; UNIPARC:UPI000017711B

C:Keywords: oxygen carrier

Query Match 20.5%; Score 41; DB 2; Length 24;

Best Local Similarity 31.6%; Pred. No. 1e+02;

Matches 6; Conservative 7; Mismatches 2; Indels 4; Gaps 1;

QY 16 QEKNEQELLELDKWNANLW 34

Db 8 EDREMQLMW----WANVWS 22

C;Date: 27-Oct-1995 #sequence revision 03-Nov-1995 #text change 03-Nov-1995

C;Accession: S56313
R;aylor, C.B.; Green, P.J.
Plant Mol. Biol. 28, 27-38, 1995
A;Title: Identification and characterization of genes with unstable transcripts (GUTs) in
A;Reference number: S56313; MUID:95306789; PMID:7787185
A;Accession: S56313
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-44 <TAY>
A;Cross-references: UNIPARC:UPI000017B0A6

```
Query Match      18.5%; Score 37; DB 2; Length 44;
Best Local Similarity 19.4%; Pred. NO. 6e+02;
Matches 6; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
```

Qy	5	IYNLL	EESQN	QEQKE	NQEQLLEL	LDKWANLW	NNW	35
	:	:	:	:	:	:	:	
Db	2	VKRILQ	EYKEMO	SQNSP	DDFMS	PLEENIFEW	32	
	:	:	:	:	:	:	:	

RESULT 9

S77793
transketolase [EC 2.2.1.1] - Mycoplasma capricolium (fragment)
N;Alternate names: protein MC315
C;Species: Mycoplasma capricolium
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S77793
R;Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.; Mol. Microbiol. 16, 955-967, 1995
A;Title: Exploring the Mycoplasma capricolium genome: a minimal cell reveals its physiological
A;Reference number: S77739; MUID:96059641; PMID:7476192
A;Accession: S77793
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-40 <BOR>
A;Cross-references: UNIPROT:Q49047; UNIPARC:UPI00000B7B19; EMBL:Z33230; NID:g514477; PDB:1Y87
A;Experimental source: ATCC 27343
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: transketolase; thiamin pyrophosphate-binding domain homology
C;Keywords: transpherase

Query Match 18.2%; Score 36.5; DB 2; Length 40;
Best Local Similarity 34.5%; Pred. NO. 6.2e+02;
Matches 10; Conservative 2; Mismatches 10; Indels 7; Gaps 1;

```

QY      3  GIIYNLLEESQOQEKNEQELLELDKWAN 31
      ||||| : | || : | |
Db      2  GIIYVLNKIMNENPKNPE-----WEN 23

```

RESULT 10

I46523 troponin T 4f - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
 C:Accession: I46523
 R:Briggs, M.M.; Lin, J.J.; Schachet, F.H.
 J. Muscle Res. Cell. Motil. 8, 1-12, 1987
 A:Title: The extent of amino-terminal heterogeneity in rabbit fast skeletal muscle troponin
 A:Reference number: I46522; MID:87251333; PMID:2439538
 A:Accession: I46523
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-32 <BRI>
 A:Cross-references: UNIPARC:UPI000016C510; EMBL:U04978; NID:g440816; PIDN:AAA16031.1; PI
 C:Superfamily: troponin T

```
Query Match      18.0%; Score 36; DB 2; Length 32;
Best Local Similarity 46.2%; Pred. No. 5.5e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      10 EESQNQKEKNEQE 22  
        |||:|:|:|:|:  
Db      11 EEAQEEEEVHEEE 23
```

RESULT 11

I66797
troponin T 3f - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: I66797
E;Briggs, M.M.; Schachat, F.
Dev. Biol. 138, 503-509, 1993
A/Title: Origin of fetal troponin T: Developmentally regulated splicing of
A/Reference number: I53073; MUID:93345743; PMID:834466
A/Accession: I66797
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-38 <RES>
A/Cross-references: UNIPROT:Q62620; UNIPARC:UPI00000E7D00; EMBL:U04981; NID
C/Sequencefamily: troponin T

	Query Match	18.0%;
	Best Local Similarity	41.2%;
	Matches	7; Conservative
Qy	6 YNLLSESNQKNEQEE	22
	::: :	
Db	13 YEEEEEQEEEEVEEEE	29

RESULT 12

T48342

hypothetical protein F15A17.240 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2002
C:Accession: T48342

R.; Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Daseville, R.; Des-
ewes, H.M.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24491

A:Accession: T48342

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-41 <BEV>

A:Cross-references: UNIPROT:Q9LWY4; UNIPARC:UPI000000AA77A; EMBL:AL163002

A:Experimental source: cultivar Columbia; BAC clone F15A17

C:Genetics:

A:Map position: 5

A:Note: F15A17.240

Query Match 18.0%; Score 36; DB 2; Length 41;
Best Local Similarity 31.6%; Pred. No. 7.3e+02;
Matches 6; Conservative 6; Mismatches 7; Indels 0;
Gaps 0;

QY 4 I IYNLLEESQNQEKNEQE 22
| : : || : : : ||
pB 19 ILETILEGGETEEDNOEOE 37

RESULT 13

troponin T3f, fast skeletal muscle - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S74261
 R:Briggs, M.M.; Maready, M.; Schmidt, J.M.; Schachar, F.
 FEBS Lett. 350, 37-40, 1994
 A:Title: Identification of a fetal exon in the human fast Troponin T gene.
 A:Reference number: S48660; MUID:94341369; PMID:8062920
 A:Accession: S74261
 A:Molecule type: mRNA

A:Residues: 1-48 <BRI>
A:Cross-references: UNIPROT:P45378; UNIPARC:UPI00000711F8; EMBL:U14644; NID:G557029; PID
C:Superfamily: troponin T
C:Keywords: alternative splicing; phosphoprotein; skeletal muscle

Query Match 18.0%; Score 36; DB 2; Length 48;
Best Local Similarity 41.2%; Pred. No. 8.7e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 6 YNLEESNQKNEQE 22
DB 13 YEEEAQEEVEVEE 29

RESULT 14
T06923
high light-inducible protein homolog - Cyanophora paradoxa cyanelle
C:Species: cyanelle Cyanophora paradoxa
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06923
R:Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.
submitted to the EMBL Data Library, July 1995
A:Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
A:Reference number: Z15840
A:Accession: T06923
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-49 <STI>
A:Cross-references: UNIPROT:P48367; UNIPARC:UPI000013A441; EMBL:U30821; NID:G1016083; PID
A:Experimental source: strain Pringsheim LB555
C:Genetics:
A:Gene: ycf17
A:Genome: cyanelle
C:Superfamily: high light-inducible protein ss12542
C:Keywords: cyanelle

Query Match 18.0%; Score 36; DB 2; Length 49;
Best Local Similarity 80.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 31 NLWNW 35
DB 6 NIWNW 10
RESULT 15
I77411
renin-2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C:Accession: I77411
R:Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.W.
Mol. Cell. Biol. 4, 2321-2331, 1984
A:Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analysis
A:Reference number: I57576; MUID:85085936; PMID:6392850
A:Accession: I77411
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-30 <RES>
A:Cross-references: UNIPROT:P00796; UNIPARC:UPI000016C94B; GB:K02801; NID:G200695; PID:
C:Superfamily: Pepsin

Query Match 17.5%; Score 35; DB 2; Length 30;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 WANLWNW 35
DB 9 WALLWLW 15

Search completed: March 6, 2006, 15:44:16
Job time : 19.3333 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:31:50 ; Search time 116.667 Seconds
(without alignments)
217.706 Million cell updates/sec

Title: US-09-809-060A-3
Perfect score: 200
Sequence: 1 YTGIIYNLEESQKNEQKLELDKWLNNWF 36

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

*Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 90886

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	192	96.0	Q69898_9HIV1	Q69898 human immun
2	186	93.0	Q69900_9HIV1	Q69900 human immun
3	183	91.5	Q69909_9HIV1	Q69909 human immun
4	180	90.0	Q69899_9HIV1	Q69899 human immun
5	179	89.5	Q69910_9HIV1	Q69910 human immun
6	178	89.0	Q69895_9HIV1	Q69895 human immun
7	178	89.0	Q69896_9HIV1	Q69896 human immun
8	176	88.0	Q69908_9HIV1	Q69908 human immun
9	174	87.0	Q69907_9HIV1	Q69907 human immun
10	171	85.5	Q69905_9HIV1	Q69905 human immun
11	169	84.5	Q69906_9HIV1	Q69906 human immun
12	168	84.0	Q69899_9HIV1	Q69899 human immun
13	166	83.0	Q69893_9HIV1	Q69893 human immun
14	166	83.0	Q69894_9HIV1	Q69894 human immun
15	164	82.0	Q69892_9HIV1	Q69892 human immun
16	163	81.5	Q69903_9HIV1	Q69903 human immun
17	163	81.5	Q69904_9HIV1	Q69904 human immun
18	150	75.0	Q69897_9HIV1	Q69897 human immun
19	143	71.5	Q69901_9HIV1	Q69901 human immun
20	143	71.5	Q69902_9HIV1	Q69902 human immun
21	50	25.0	Q9MC62_BPD3	Q9MC62 bacterioph
22	48	24.0	Q9XXW6_NEOP	Q9XXW6 nautilerme
23	48	24.0	Q4HNW1_CAMP	Q4HNW1 campylobact
24	45.5	22.8	Q5KLF8_CRYNE	Q5KLF8 cryptococcu
25	45	22.5	Q5Q1L8_CRIGR	Q5Q1L8 cricetulus
26	44	22.0	Q04241_9POXV	Q04241 vaccinia vi
27	43	21.5	Q7S912_NEUCR	Q7S912 neurospora
28	43	21.5	Q905J7_9HIV1	Q905J7 human immun
29	43	21.5	Q4T4H4_TENG	Q4T4H4 tetraodon n
30	42	21.0	Q90RH9_9HIV1	Q90RH9 human immun
31	42	21.0	Y260_BACHD	Q9K953 bacillus ha

32	42	21.0	36	2	Q905E1_9HIV1	Q905E1 human immun
33	42	21.0	36	2	Q905E9_9HIV1	Q905E9 human immun
34	42	21.0	36	2	Q905I1_9HIV1	Q905I1 human immun
35	42	21.0	45	2	Q8L6Q9_GOSHI	Q8L6Q9 gosyypium h
36	42	21.0	46	2	Q8L6Q8_GOSHI	Q8L6Q8 gosyypium h
37	42	21.0	47	2	Q55BR3_DICDI	Q55BR3 dictyoasteli
38	42	21.0	50	2	Q8L6Q7_GOSHI	Q8L6Q7 gosyypium h
39	41.5	20.8	30	2	Q675B2_MOUSE	Q675B2 mus musculu
40	41.5	20.8	50	2	Q6SKY9_9CRUS	Q6SKY9 speleoneocte
41	41	20.5	39	2	Q5XCP1_STRP6	Q5XCP1 streptococ
42	41	20.5	42	2	Q9TWS6_LAMSP	Q9TWS6 lamellibrac
43	41	20.5	47	2	Q4MNY6_BACCE	Q4MNY6 bacillus ce
44	41	20.5	47	2	Q7J0N7_BACCI	Q7J0N7 bacillus ce
45	41	20.5	47	2	Q818G2_BACCR	Q818G2 bacillus ce

ALIGNMENTS

RESULT 1
Q69898_9HIV1
ID Q69898_9HIV1 PRELIMINARY; PRT; 50 AA.
AC Q69898;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2FS, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06728; AA19141.1; -; mRNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; Gp41; 1.
FT NON_TER 1 50
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 6358 MW; EABA093A1C6C79E1 CRC64;
Query Match 96.0%; Score 192; DB 2; Length 50;
Best Local Similarity 94.4%; Pred. No. 5.6e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YTGIIYNLEESQKNEQKLELDKWLNNWF 36
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Db 15 YTGIIYNLEESQKNEQKLELDKWLNNWF 50
RESULT 2
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ID Q69900_9HIV1 PRELIMINARY; PRT; 50 AA.
AC Q69900;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;


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RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06737; AAA19150.1; -; mRNA.
DR HSSP; O87973; 2SIV.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
FT NON_TER 50
SQ SEQUENCE 49 AA; 6241 MW; 29C4E5A8C7CDD8 CRC64;

Query Match 87.0%; Score 174; DB 2; Length 49;
Best Local Similarity 83.3%; Pred. No. 6.9e-13;
Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db 14 YTSIIYTLLEESQKQKNEQELLELDKWNWLF 49

RESULT 10
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AC Q69905;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06735; AAA19148.1; -; mRNA.
DR HSSP; F31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 34
FT NON_TER 35
SQ SEQUENCE 34 AA; 4196 MW; 7B724A8EA164BD9C CRC64;

Query Match 85.5%; Score 171; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 1e-12;
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GIIYNLEESQKQKNEQELLELDKWNWLF 36
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Db 1 GLIYTLLEKSNQKQKNEQELLELDKWNWLF 34

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AC Q69906;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06736; AAA19149.1; -; mRNA.
DR HSSP; F31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
FT NON_TER 50
SQ SEQUENCE 49 AA; 6214 MW; 29C4E5A8C8BD63DD8 CRC64;

Query Match 84.5%; Score 169; DB 2; Length 49;
Best Local Similarity 80.6%; Pred. No. 2.6e-12;
Matches 29; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQKQKNEQELLELDKWNWLF 36
|||:|||||:|||||:|||||:|||||:|||||
Db 14 YTSIIYTLLEESQKQKNEQELLELDKWNWLF 49

RESULT 12
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AC Q69891;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06721; AAA19134.1; -; mRNA.
DR HSSP; F31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
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FT NON_TER 42
SQ SEQUENCE 41 AA; 5082 MW; 0B9C7E2CDD403CC6 CRC64;

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Query Match      84.0%; Score 168; DB 2; Length 41;
Best Local Similarity 88.2%; Pred. No. 2.8e-12;
Matches 30; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GIIYNLIETSNQOQKNEQELLELDKWASLWNWF 34

RESULT 13
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ID Q69893_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69893;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06723; AAA19136.1; -; mRNA.
DR HSSP; P31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1
FT NON TER 34
SQ SEQUENCE 34 AA; 4196 MW; 0C7CAA60A164B89C CRC64;

Query Match      83.0%; Score 166; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 3.9e-12;
Matches 30; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GIIYNLEESQNOQKNEQELLELDKWANLWNWF 36
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RESULT 14
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ID Q69894_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69894;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
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SQ SEQUENCE 34 AA; 4182 MW; A37CAA60A164AEF0 CRC64;

Query Match      83.0%; Score 166; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 3.9e-12;
Matches 30; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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AC Q69892;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
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DR Pfam; PF00517; GP41; 1.
FT NON TER 1
FT NON TER 41
SQ SEQUENCE 41 AA; 5081 MW; 0B9C70CC33403CC6 CRC64;

Query Match      82.0%; Score 164; DB 2; Length 41;
Best Local Similarity 85.3%; Pred. No. 8.3e-12;
Matches 29; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GIIYNLEESQNOQKNEQELLELDKWANLWNWF 36
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GenCore version 5.1.7
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OM protein - protein search, using sw model

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(without alignments)
107.578 Million cell updates/sec

Title: US-09-809-060A-3
Perfect score: 200
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	200	100.0	36	2	US-08-486-099-4
3	200	100.0	36	2	US-08-360-107A-4
4	200	100.0	36	2	US-08-484-223B-4
5	200	100.0	36	2	US-08-919-597-4
6	200	100.0	36	2	US-08-475-668A-4
7	200	100.0	36	2	US-08-485-551A-4
8	200	100.0	36	2	US-08-471-913A-4
9	200	100.0	36	2	US-08-554-616-4
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13	200	100.0	36	2	US-08-474-349A-4
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25	200	100.0	36	2	US-09-350-641C-1359
26	200	100.0	36	2	US-09-350-841A-1358
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28 200 100.0 36 2 US-08-487-266A-4 Sequence 4, Appli
29 200 100.0 36 2 US-09-623-548A-1422 Sequence 1422, Ap
30 200 100.0 36 2 US-10-252-136-4 Sequence 4, Appli
31 200 100.0 36 2 US-09-657-276-1422 Sequence 1422, Ap
32 200 100.0 36 2 US-08-484-741-4 Sequence 4, Appli
33 184 92.0 36 1 US-08-073-028-3 Sequence 3, Appli
34 184 92.0 36 2 US-08-360-107A-3 Sequence 3, Appli
35 184 92.0 36 2 US-08-554-616-3 Sequence 1543, Ap
36 184 92.0 36 2 US-09-350-841A-1543 Sequence 110, App
37 182 91.0 46 2 US-08-965-056-110 Sequence 110, App
38 180 90.0 36 2 US-09-082-279B-642 Sequence 642, App
39 180 90.0 36 2 US-09-315-304B-642 Sequence 642, App
40 180 90.0 36 2 US-09-834-784-642 Sequence 642, App
41 180 90.0 36 2 US-09-515-965A-642 Sequence 642, App
42 180 90.0 36 2 US-09-350-641C-642 Sequence 642, App
43 180 90.0 36 2 US-09-350-841A-642 Sequence 642, App
44 178 89.0 36 2 US-08-486-099-3 Sequence 3, Appli
45 178 89.0 36 2 US-08-484-223B-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-073-028-4
; Sequence 4, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-073-028-4

Query Match 100.0%; Score 200; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQKNEQKNEQELLELDKQANLWVNF 36
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Db 1 YTGIIYNLLEESQKNEQKNEQELLELDKWANLWNWF 36

RESULT 2

US-08-486-099-4

; Sequence 4, Application US/08486099

; Patent No. 6013263

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

; TITLE OF INVENTION: B VIRUS TRANSMISSION

; NUMBER OF SEQUENCES: 209

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,099

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEX: 66141 PENNIE

; TELEFAX: (212) 869-9741/8864

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-486-099-4

Query Match 100.0%; Score 200; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 4.6e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQKNEQKNEQELLELDKWANLWNWF 36

Db 1 YTGIIYNLLEESQKNEQKNEQELLELDKWANLWNWF 36

RESULT 3

US-08-360-107A-4

; Sequence 4, Application US/08360107A

; Patent No. 6017536

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

; TITLE OF INVENTION: TRANSMISSION

; NUMBER OF SEQUENCES: 149

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/360,107A

; FILING DATE: 20-DEC-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-013

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-360-107A-4

Query Match

Best Local Similarity 100.0%; Score 200; DB 2; Length 36;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQKNEQKNEQELLELDKWANLWNWF 36

Db 1 YTGIIYNLLEESQKNEQKNEQELLELDKWANLWNWF 36

RESULT 4

US-08-484-223B-4

; Sequence 4, Application US/08484223B

; Patent No. 6020459

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

; TITLE OF INVENTION: TRANSMISSION

; NUMBER OF SEQUENCES: 245

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/484,223B
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-4

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 5

US-08-919-597-4
Sequence 4, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-4

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 6

US-08-475-668A-4
Sequence 4, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-4

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

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RESULT 7
US-08-485-551A-4
; Sequence 4, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-485-551A-4

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEQELLELDKQWNLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |
Db 1 YTGIIYNLLEESONQOEKNEQELLELDKQWNLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-08-471-913A-4
; Sequence 4, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
```

```
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-471-913A-4

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEQELLELDKQWNLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |
Db 1 YTGIIYNLLEESONQOEKNEQELLELDKQWNLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |

RESULT 9
US-08-554-616-4
; Sequence 4, Application US/08554616
; Patent No. 6133418
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,616
; FILING DATE: 06-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,028
; FILING DATE: 07-JUN-1993
```

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-554-616-4

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 10
US-08-485-264A-4
Sequence 4, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-485-264A-4

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 11
US-09-082-279B-1358
Sequence 1358, Application US/09082279B
Patent No. 6256782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1358
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-1358

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 12
US-09-082-279B-1359
Sequence 1359, Application US/09082279B
Patent No. 6256782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1359
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-1359

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLESQKQKNEQELLELDKQWLNWNF 36
Db 1 YTGIIYNLLESQKQKNEQELLELDKQWLNWNF 36

RESULT 13

US-08-474-349A-4
; Sequence 4, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-4

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLESQKQKNEQELLELDKQWLNWNF 36
Db 1 YTGIIYNLLESQKQKNEQELLELDKQWLNWNF 36

RESULT 14

US-09-315-304B-1358
; Sequence 1358, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merytka, G.
; APPLICANT: Anwer, M.

; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1358
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1358

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YTGIIYNLLESQKQKNEQELLELDKQWLNWNF 36
Db 1 YTGIIYNLLESQKQKNEQELLELDKQWLNWNF 36

RESULT 15

US-09-315-304B-1359
; Sequence 1359, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merytka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1359
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1359

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YTGIIYNLLESQKQKNEQELLELDKQWLNWNF 36
Db 1 YTGIIYNLLESQKQKNEQELLELDKQWLNWNF 36

Search completed: March 6, 2006, 15:45:44
Job time : 27.6667 secs

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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:44:30 ; Search time 94 Seconds
(without alignments)
160.020 Million cell updates/sec

Title: US-09-809-060A-3
Perfect score: 200
Sequence: 1 YTGIIYNLLEESQKNEQKNEQELLELDKQWLNWNF 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 549595

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pap:*
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6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	100.0	36	3	US-09-809-060-3
2	200	100.0	36	4	US-10-252-136-4
3	200	100.0	36	4	US-10-351-641-1358
4	200	100.0	36	4	US-10-351-641-1359
5	200	100.0	36	4	US-10-267-682-4
6	200	100.0	36	4	US-10-267-748-4
7	200	100.0	36	4	US-10-663-589-39
8	200	100.0	36	4	US-10-671-282-39
9	200	100.0	36	5	US-10-168-295-4
10	200	100.0	36	5	US-10-950-010-4
11	200	100.0	36	6	US-11-066-697-1422
12	182	91.0	46	3	US-09-854-816-110
13	181	90.5	36	5	US-10-950-010-534
14	180	90.0	36	4	US-10-351-641-642
15	180	90.0	36	4	US-10-457-780-52
16	180	90.0	36	5	US-10-950-010-537
17	180	90.0	36	5	US-10-950-010-539
18	178	89.0	36	3	US-09-809-060-2
19	178	89.0	36	4	US-10-352-136-3
20	178	89.0	36	4	US-10-351-641-1357
21	178	89.0	36	4	US-10-267-682-3
22	178	89.0	36	4	US-10-267-748-3
23	178	89.0	36	4	US-10-663-589-38
24	178	89.0	36	4	US-10-671-282-38
25	178	89.0	36	5	US-10-168-295-3
26	178	89.0	36	5	US-10-950-010-3
27	178	89.0	36	6	US-11-066-697-1421

28 178 89.0 46 3 US-09-854-816-109 Sequence 109, App
29 177 88.5 36 4 US-10-351-641-856 Sequence 856, App
30 177 88.5 36 5 US-10-950-010-536 Sequence 536, App
31 177 88.0 36 5 US-10-950-010-541 Sequence 541, App
32 176 88.0 36 3 US-09-809-060-19 Sequence 19, Appl
33 176 88.0 36 3 US-09-779-451-44 Sequence 44, Appl
34 176 88.0 36 4 US-10-351-641-1051 Sequence 1051, Ap
35 176 88.0 36 4 US-10-685-801-44 Sequence 44, Appl
36 176 88.0 36 4 US-10-660-206-44 Sequence 44, Appl
37 176 88.0 46 3 US-09-809-060-17 Sequence 17, Appl
38 176 88.0 46 3 US-09-779-451-42 Sequence 42, Appl
39 176 88.0 46 4 US-10-685-801-42 Sequence 42, Appl
40 176 88.0 46 4 US-10-660-206-42 Sequence 42, Appl
41 175 87.5 36 3 US-09-809-060-1 Sequence 1, Appl
42 175 87.5 36 3 US-09-809-060-85 Sequence 85, Appl
43 175 87.5 36 3 US-09-796-202-10 Sequence 10, Appl
44 175 87.5 36 3 US-09-960-717-2 Sequence 2, Appl
45 175 87.5 36 3 US-09-779-451-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-809-060-3
; Sequence 3, Application US/09809060
; Publication NO. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; TITLE OF INVENTION: Regions of HIV Envelope Proteins
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-3

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Best Local Similarity 100.0%; Pred. No. 2.6e-16; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0;
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Db 1 YTGIIYNLLEESQKNEQKNEQELLELDKQWLNWNF 36

RESULT 2
US-10-252-136-4
; Sequence 4, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

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; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-4

Query Match      100.0%; Score 200; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YTGIIYNLLEESQOQEKNEQELLELDKWANLWNWF 36

RESULT 3
US-10-351-641-1358
; Sequence 1358, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1358
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1358

Query Match      100.0%; Score 200; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YTGIIYNLLEESQOQEKNEQELLELDKWANLWNWF 36

RESULT 4
US-10-351-641-1359
; Sequence 1359, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; ;

; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1359
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-252-136-4

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Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YTGIIYNLLEESQOQEKNEQELLELDKWANLWNWF 36

RESULT 5
US-10-267-682-4
; Sequence 4, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-267-682-4
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Query Match 100.0%; Score 200; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 6
US-10-267-748-4
; Sequence 4, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-267-748-4

Query Match 100.0%; Score 200; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 7

US-10-663-589-39
; Sequence 39, Application US/10663589
; Publication No. US20040063637A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 39
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-39

Query Match 100.0%; Score 200; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 8
US-10-671-282-39
; Sequence 39, Application US/10671282
; Publication No. US20040122214A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
; FILE REFERENCE: TRM-004
; CURRENT APPLICATION NUMBER: US/10/671,282
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/414,439
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 39
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-671-282-39

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Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 9
US-10-168-295-4
; Sequence 4, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Baroudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19

; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-4

Query Match 100.0%; Score 200; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 10
US-10-950-010-4
; Sequence 4, Application US/10950010
; Publication No. US20050070475A1
; GENERAL INFORMATION:
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: DUFRESNE, Robert S.
; APPLICANT: BOUDJELLAB, Niesab
; APPLICANT: ROBITAILLE, Martin
; APPLICANT: MILNER, Peter G.
; TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL
; FILE OF INVENTION: INFECTION
; FILE REFERENCE: 500862001501/REDC-1512
; CURRENT APPLICATION NUMBER: US/10/950,010
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: US 09/623,533
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13651
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: US 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/153,406
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-950-010-4

Query Match 100.0%; Score 200; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
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DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 11
US-11-066-697-1422
; Sequence 1422, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmés, Darreh L.

; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1422
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1422

Query Match 100.0%; Score 200; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
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DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 12
US-09-854-816-110
; Sequence 110, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovaanik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	175	87.5	36	6	US-10-841-956A-1	Sequence 1, Appli
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3	175	87.5	36	7	US-11-187-687-22	Sequence 22, Appl
4	175	87.5	34	7	US-11-112-277-33	Sequence 33, Appl
5	175	87.5	47	7	US-11-187-687-24	Sequence 24, Appl
6	163	81.5	44	7	US-11-089-426-10	Sequence 10, Appl
7	138	69.0	36	6	US-10-506-796A-6	Sequence 6, Appli
8	137	68.5	36	6	US-10-506-796A-5	Sequence 5, Appli
9	135	67.5	36	6	US-10-506-796A-7	Sequence 7, Appli
10	132	66.0	35	6	US-10-506-796A-1	Sequence 1, Appli
11	132	66.0	36	6	US-10-506-796A-3	Sequence 3, Appli
12	120	60.0	36	6	US-10-506-796A-4	Sequence 4, Appli
13	119	59.5	39	6	US-10-841-956A-3	Sequence 3, Appli
14	119	59.5	39	7	US-11-029-003-3	Sequence 3, Appli
15	119	59.5	40	7	US-11-112-277-34	Sequence 34, Appli
16	106	53.0	38	7	US-11-151-598-4	Sequence 4, Appli
17	101	50.5	34	7	US-11-112-277-6	Sequence 6, Appli
18	101	50.5	34	7	US-11-112-277-38	Sequence 38, Appli
19	101	50.5	34	7	US-11-151-598-10	Sequence 10, Appl
20	101	50.5	34	7	US-11-151-598-12	Sequence 12, Appl
21	101	50.5	35	7	US-11-112-277-7	Sequence 7, Appli
22	101	50.5	35	7	US-11-112-277-37	Sequence 37, Appli
23	101	50.5	47	7	US-11-151-598-5	Sequence 5, Appli
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25	100	50.0	34	7	US-11-112-277-36	Sequence 36, Appli

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RESULT 2
US-11-029-003-1
; Sequence 1, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEL, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029,003
; CURRENT FILING DATE: 2005-01-05

```


RESULT 8
US-10-506-796A-5
; Sequence 5, Application US/10508796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir

RESULT 10
US-10-506-796A-1
; Sequence 1; Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:

```
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(35)
; OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
US-10-506-796A-1

Query Match          66.0%; Score 132; DB 6; Length 35;
Best Local Similarity 92.0%; Pred. No. 3.2e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 SQOQEKNEQELLELDKRWANLWNWF 36
Db 1 SQTQEKNEQELLELDKRWASLWNWF 25

RESULT 11
US-10-506-796A-3
; Sequence 3, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-506-796A-3

Query Match          66.0%; Score 132; DB 6; Length 36;
Best Local Similarity 92.0%; Pred. No. 3.3e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 SQOQEKNEQELLELDKRWANLWNWF 36
Db 2 SQTQEKNEQELLELDKRWASLWNWF 26

RESULT 12
US-10-506-796A-4
; Sequence 4, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
```

```
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(35)
; OTHER INFORMATION: HIV-1 isolate MN clone v5 (residues 649-685)
US-10-506-796A-4

Query Match          60.0%; Score 120; DB 6; Length 36;
Best Local Similarity 84.0%; Pred. No. 9.8e-09;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 SQOQEKNEQELLELDKRWANLWNWF 36
Db 1 SQTQEKNEQELLELDKRWESLWNWF 25

RESULT 13
US-10-841-956A-3
; Sequence 3, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-3

Query Match          59.5%; Score 119; DB 6; Length 39;
Best Local Similarity 72.4%; Pred. No. 1.4e-08;
Matches 21; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 8 LLEBSQOQEKNEQELLELDKRWANLWNWF 36
Db 11 LLEQAQIQOQEKNEYELQKLDKRWASLWNWF 39

RESULT 14
US-11-029-003-3
; Sequence 3, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEL, JAMES
```

; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS

```
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029,003
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539,207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487,964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469,600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-029-003-3
```

```
Query Match 59.5%; Score 119; DB 7; Length 39;
Best Local Similarity 72.4%; Pred. No. 1.4e-08;
Matches 21; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 8 LLEESQOQEKNEQELLELDKWANLWNWF 36
| | | | | | | | | | | | | | | | | |
Db 11 LLEQAQIQOQEKNEYELQKLDKWASLWFW 39
```

RESULT 15

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US-11-112-277-34
; Sequence 34, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T1249 Analogue
; NAME/KEY: MOD_RES
; LOCATION: 40
; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-34
```

```
Query Match 59.5%; Score 119; DB 7; Length 40;
Best Local Similarity 72.4%; Pred. No. 1.5e-08;
Matches 21; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 8 LLEESQOQEKNEQELLELDKWANLWNWF 36
| | | | | | | | | | | | | | | | | |
Db 11 LLEQAQIQOQEKNEYELQKLDKWASLWFW 39
```

Search completed: March 6, 2006, 15:54:21
Job time : 10 secs

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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:12:57 ; Search time 117.333 Seconds
(without alignments)
134.809 Million cell updates/sec

Title: US-09-809-060A-3
Perfect score: 36
Sequence: 1 YGIIYNLLESQKQKNEQLLELDKWNLWVF 36

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 2443163 seqs, 439378781 residues

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: Geneseq1980s.*
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3: Geneseq2000s.*
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6: Geneseq2003s.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	36	2	AAR67699 DP-178 ho
2	36	100.0	36	2	AAR98400 Peptide c
3	36	100.0	36	2	AAR17013 DP-178-li
4	36	100.0	36	4	AAB54787 HIV antiv
5	36	100.0	36	4	AAB52246 Virus rel
6	36	100.0	36	4	AAB78239 Core poly
7	36	100.0	36	4	AAB78240 Core poly
8	36	100.0	36	4	AAB70181 HIV viral
9	36	100.0	36	4	ABB02832 Viral cor
10	36	100.0	36	4	ABB02831 Viral cor
11	36	100.0	36	4	ABG67041 HIV-1 gp4
12	36	100.0	36	4	ABB01246 Viral DPl
13	36	100.0	36	4	ABB01247 Viral DPl
14	36	100.0	36	4	AAU13793 DP178-lik
15	36	100.0	36	4	AAU13792 DP178-lik
16	36	100.0	36	4	AAU14013 DP178 hom
17	36	100.0	36	5	AAU18773 HIV gp41
18	36	100.0	36	5	AAU02851 Hybrid po
19	36	100.0	36	5	AAU02852 Hybrid po
20	36	100.0	36	6	ABO10165 HIV1-RF g
21	36	100.0	36	8	ADN06924 Peptide #
22	36	100.0	36	8	ADS87259 HIV-1 gp4
23	36	100.0	36	9	ADY71494 HIV-1 tra
24	36	100.0	269	2	AAU22837 SEQ ID NO

25	36	100.0	269	5	ABG68308 Envelope
26	36	100.0	269	6	ABU57715 Human imm
27	36	100.0	861	2	AAW43074 HIV-1 gp1
28	36	100.0	865	1	ADP70175 Sequence
29	36	100.0	865	9	ADX39688 HIV Env p
30	36	100.0	866	1	ADP80966 HIV prote
31	31	86.1	35	3	AAU89838 Core poly
32	31	86.1	35	3	AAU89839 Core poly
33	27	75.0	225	8	ADU68214 gp41 ecto
34	27	75.0	849	9	ADX39678 HIV Env p
35	26	72.2	36	2	AAR67698 DP-178 ho
36	26	72.2	36	2	AAR98399 DP185 cor
37	26	72.2	36	2	AAU17012 DP-178-li
38	26	72.2	36	4	AAU67040 HIV-1 gp4
39	26	72.2	36	4	AAU14012 DP178 hom
40	26	72.2	38	7	ADK66257 Human imm
41	26	72.2	45	7	ADK66261 Human imm
42	26	72.2	48	8	ADU80506 Transmemb
43	26	72.2	48	9	ADZ40264 HIV-1 gp4
44	26	72.2	856	1	AAU61514 Sequence
45	26	72.2	856	2	AAW89325 HIV-1 env

ALIGNMENTS

RESULT 1

AAR67699
ID AAR67699 standard; peptide; 36 AA.
XX AAR67699;
AC AAR67699;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 24-AUG-1995 (first entry)
XX
DE DP-178 homologue derived from HIV-1 RF has antiviral activity.
XX
KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
KW human immunodeficiency virus; transmembrane protein; gp41; alpha helix;
KW leucine zipper; DP-185.
XX
OS Human immunodeficiency virus; (RF isolate).
XX
PN W09428920-A1.
XX
PD 22-DEC-1994.
XX
PF 07-JUN-1994; 94WO-US005739.
PR
XX
PR 07-JUN-1993; 93US-00073028.
PA (UYDU-) UNIV DUKE.
XX
PI Bolognesi DP, Matthews TJ, Wild CT, Barney SO, Lambert DM;
PI Petteway SR;
XX
DR WPI; 1995-036105/05.
XX
XX
PT Computer search generated synthetic peptides - are inhibitors of HIV transmission.
PT
XX
PS Example; Fig 1; 182pp; English.
XX
CC This peptide is isolated from HIV-1 isolate RF, and is a homologue of the
CC peptide DP-178. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
CC isolate LAI transmembrane protein gp41. It forms a putative alpha helix
CC at the C-terminal end of the gp41 ectodomain, and complexes with DP-107
CC (corresponds to amino acids 558-595) which contains a leucine zipper
CC motif. The peptides complex via non-covalent protein-protein
CC interactions, and possess anti-viral activity. The peptide inhibits
CC transmission to uninfected cells, and can also be used as type and/or
CC subtype specific diagnostic tools. (Updated on 25-MAR-2003 to correct PN

CC field.) (Updated on 16-OCT-2003 to standardise OS field)

```
XX SQ Sequence 36 AA;
Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 2
AAR98400
ID AAR98400 standard; peptide; 36 AA.
XX AAR98400;
XX
XX 16-OCT-2003 (revised)
DT 17-FEB-1997 (first entry)
XX
DE Peptide corresponding to residues 638-673 of HIV-1(RF) gp41.
XX
KW Antifusogenic activity; antiviral capability; coiled-coil peptide;
KW ALLMOTI5; 107x178x4; PLZIP search motif; viral transmission; HIV;
KW influenza virus; hepatitis B virus.
XX
OS Human immunodeficiency virus 1.
XX
XX WO9619495-A1.
PN
XX
XX 27-JUN-1996.
PD
XX
XX 20-DEC-1995; 95WO-US016733.
PF
XX
XX 20-DEC-1994; 94US-00360107.
PR
XX 06-JUN-1995; 95US-00470896.
XX
XX (UYDU-) UNIV DUKE.
PA
XX (TRIM-) TRIMERIS INC.
PA
XX Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;
PI Petteway SR, Langlois AJ;
XX WPI; 1996-309517/31.
DR
XX
XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
PT isolated peptide recognised by an ALLMOTI5, 107x178x4 or PLZIP sequence
PT search motif.
XX
XX Disclosure; Fig 1; 471pp; English.
PS
XX
XX The sequences given in AAR98398-408 represent peptides which exhibit
CC antifusogenic activity, antiviral capability and/or the ability to
CC modulate intracellular processes involving coiled-coil peptide
CC structures. These peptides are recognised by the ALLMOTI5, 107x178x4 and
CC PLZIP search motifs. These peptides may be used to inhibit the
CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
XX virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 36 AA;
Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 3
AAR98400
ID AAR98400 standard; peptide; 36 AA.
XX AAR98400;
XX
XX 16-OCT-2003 (revised)
DT 17-FEB-1997 (first entry)
XX
DE Peptide corresponding to residues 638-673 of HIV-1(RF) gp41.
XX
KW Antifusogenic activity; antiviral capability; coiled-coil peptide;
KW ALLMOTI5; 107x178x4; PLZIP search motif; viral transmission; HIV;
KW influenza virus; hepatitis B virus.
XX
OS Human immunodeficiency virus 1.
XX
XX WO9619495-A1.
PN
XX
XX 27-JUN-1996.
PD
XX
XX 20-DEC-1995; 95WO-US016733.
PF
XX
XX 20-DEC-1994; 94US-00360107.
PR
XX 06-JUN-1995; 95US-00470896.
XX
XX (UYDU-) UNIV DUKE.
PA
XX (TRIM-) TRIMERIS INC.
PA
XX Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;
PI Petteway SR, Langlois AJ;
XX WPI; 1996-309517/31.
DR
XX
XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
PT isolated peptide recognised by an ALLMOTI5, 107x178x4 or PLZIP sequence
PT search motif.
XX
XX Disclosure; Fig 1; 471pp; English.
PS
XX
XX The sequences given in AAR98398-408 represent peptides which exhibit
CC antifusogenic activity, antiviral capability and/or the ability to
CC modulate intracellular processes involving coiled-coil peptide
CC structures. These peptides are recognised by the ALLMOTI5, 107x178x4 and
CC PLZIP search motifs. These peptides may be used to inhibit the
CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
XX virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 36 AA;
Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 4
AAB54787
ID AAB54787 standard; peptide; 36 AA.
XX AAB54787;
XX
XX 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
DE HIV antiviral activity exhibiting peptide SEQ ID NO:4.
XX
KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
KW antifusogenic; mobile blood component; measles virus; MeV; HIV;
KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KW human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
```

```
AAW17013
ID AAW17013 standard; peptide; 36 AA.
XX
XX AAW17013;
AC
XX 17-OCT-2003 (revised)
DT 01-JUL-1997 (first entry)
XX
XX DP-178-like peptide useful for treatment of HIV infection.
DE
XX HIV; SIV; human; simian immunodeficiency virus; glycoprotein 41;
KW transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;
KW replication; transmission.
XX
XX Human immunodeficiency virus 1; RF isolate.
OS
XX WO9640191-A1.
PN
XX 19-DEC-1996.
PD
XX 06-JUN-1996; 96WO-US009499.
PF
XX 07-JUN-1995; 95US-00481957.
PR
XX (TRIM-) TRIMERIS INC.
PA
XX Johnson RM, Lambert DM;
PI
XX WPI; 1997-099886/09.
DR
XX
XX Compens. contg. DP-178 or DP-107 in combination with other therapeutic
PT agent - useful for treatment of HIV infection, esp. by inhibiting
PT replication or transmission of HIV.
XX
XX Disclosure; Fig 1; 84pp; English.
PS
XX
XX AAW17012-W17016 are DP-178 homologues that are useful in the treatment of
CC HIV infection. DP-178 is a peptide corresponding to residues 638-673 of
CC HIV type 1 glycoprotein 41 (gp41) transmembrane protein. DP-178 and its
CC derivatives/homologues are used in combination with a therapeutic agent,
CC e.g. a reverse transcriptase, viral protease, cytokine, glycosylation or
CC viral mRNA processing inhibitor or a nucleoside inhibitor. The peptides
CC work by inhibiting viral replication or inhibiting transmission. They may
CC also be used in vaccines for protecting against HIV infection. (Updated
CC on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 36 AA;
Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 4
AAB54787
ID AAB54787 standard; peptide; 36 AA.
XX AAB54787;
XX
XX 11-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
DE HIV antiviral activity exhibiting peptide SEQ ID NO:4.
XX
KW Long lasting fusion peptide inhibitor; viral infection; antiviral;
KW antifusogenic; mobile blood component; measles virus; MeV; SIV;
KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KW human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX
```

```
OS Human immunodeficiency virus 1.
XX WO200069902-A1.
XX
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013576.
XX
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX 15-OCT-1999; 99US-0159783P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX WPI; 2001-007496/01.
XX
XX A modified peptide and a reactive group which is reactive with amino
XX groups, hydroxyl groups, or thiol groups on blood components to form
XX stable covalent bonds useful for treatment of viral infections, e.g.
XX human immunodeficiency virus.
XX
XX Claim 6; Page 173-174; 211pp; English.
XX
XX The present invention describes a modified anti-viral peptide (I)
XX comprising a peptide that exhibits anti-viral activity and a reactive
XX group which is reactive with amino groups, hydroxyl groups, or thiol
XX groups on blood components to form stable covalent bonds. (I) has anti-
XX viral and anti-fusogenic activities. (I) inhibits viral infection of
XX cells by inhibiting cell-cell fusion or free virus infection or to reduce
XX the level of membrane fusion events between two or more entities, e.g.,
XX virus-cell or cell-cell, relative to the level of membrane fusion that
XX occurs in the absence of the peptide. (I) is useful in the treatment of
XX patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,
XX MeV, and SIV. (I) may be administered prophylactically to previously
XX uninfected individuals. This is useful in cases where an individual has
XX been subjected to a high risk of exposure to a virus. By bonding of long-
XX lived components of the blood, such as immunoglobulin, serum albumin, red
XX blood cells and platelets the activity is extended for days to weeks.
XX This is due to improved stability in vivo and a reduced susceptibility to
XX peptidase or protease degradation. This minimises the need for more
XX frequent, or even continual, administration of the peptides. AAB54784 to
XX AAB54431 represent peptides used in the exemplification of the present
XX invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 36 AA;
XX
XX Query Match 100.0%; Score 36; DB 4; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 2e-27;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKWANLWNWF 36
XX |||||
XX Db 1 YTGIIYNLLEESQNOQEKNEQELLELDKWANLWNWF 36
XX |||||
XX
XX RESULT 5
XX AAB92246
XX ID AAB92246 standard; peptide; 36 AA.
XX
XX AC AAB92246;
XX
XX DT 22-JUN-2001 (first entry)
XX
XX DE Virus related peptide SEQ ID NO:1422.
XX
XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimidyl; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX
XX WO200069900-A2.
XX 23-NOV-2000.
XX 17-MAY-2000; 2000WO-US013576.
XX 17-MAY-1999; 99US-0134406P.
XX 10-SEP-1999; 99US-0153406P.
XX 15-OCT-1999; 99US-0159783P.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity.
XX Disclosure; Page 662-663; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity in
XX vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention
XX
XX Sequence 36 AA;
XX
XX Query Match 100.0%; Score 36; DB 4; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 2e-27;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKWANLWNWF 36
XX |||||
XX Db 1 YTGIIYNLLEESQNOQEKNEQELLELDKWANLWNWF 36
XX |||||
XX
XX RESULT 6
XX AAB78239
XX ID AAB78239 standard; peptide; 36 AA.
XX
XX AC AAB78239;
XX
XX DT 19-APR-2001 (first entry)
XX
XX DE Core polypeptide T1407.
XX
XX KW Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
XX antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
XX fusion-related disorder; bacterial infection; viral infection.
XX
XX OS Unidentified.
XX
XX WO200103723-A1.
XX 18-JAN-2001.
XX 10-JUL-2000; 2000WO-US018772.
XX 09-JUL-1999; 99US-00350641.
XX
```

XX (TRIM-) TRIMERIS INC.
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2001-147136/15.
XX
XX New hybrid polypeptide, useful for preventing, treating and diagnosing
XX e.g. viral infections, comprises an enhancer peptide linked to a core
XX polypeptide.
XX
XX Disclosure; Page 58; 151pp; English.
XX
XX The present sequence is a core polypeptide which may be linked to an
XX enhancer peptide to form a novel hybrid polypeptide. The hybrid
XX polypeptide exhibits enhanced pharmacokinetic properties relative to
XX those exhibited by the core polypeptide when introduced into a living
XX system. It is used to increase the in vitro or ex vivo half-life of the
XX core polypeptide. The hybrid and core polypeptides can be used for
XX modulating fusogenic events and intracellular processes involving coiled-
XX coil peptide interactions. Other uses include preventing, treating and/or
XX diagnosing disorders involving fusion events (e.g. modulation of
XX neurotransmitter exchange and sperm-egg fusion), intracellular processes
XX involving coiled-coil peptides (e.g. bacterial infections) and viral
XX infections that involve cell-cell and/or virus-cell fusion (e.g. viral
XX infections caused by human immunodeficiency virus, respiratory syncytial
XX virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
XX polio virus). The enhancer peptide sequence increases the half-life and
XX reduces the clearance rate of therapeutic peptides, which increases their
XX efficacy and minimises the incidence and severity of adverse side
XX effects. In addition, this increases the sensitivity of the diagnostic
XX procedure in which they are used
XX
XX Sequence 36 AA;
XX
XX Query Match 100.0%; Score 36; DB 4; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 2e-27;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 YTGIIYNLLEESNQOEKNEQELLELDKRWANLWNWF 36
XX |||||||||||||||||||||||||||||||||||||||
XX 1 YTGIIYNLLEESNQOEKNEQELLELDKRWANLWNWF 36
XX
XX
XX RESULT 7
XX AAB78240
XX ID AAB78240 standard; peptide; 36 AA.
XX AC AAB78240;
XX DT 19-APR-2001 (first entry)
XX DE Core polypeptide T1408.
XX
XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
XX antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
XX fusion-related disorder; bacterial infection; viral infection.
XX
XX Unidentified.
XX
XX WO200103723-A1.
XX
XX 18-JAN-2001.
XX
XX 10-JUL-2000; 2000WO-US018772.
XX
XX 09-JUL-1999; 99US-00350641.
XX
XX (TRIM-) TRIMERIS INC.
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2001-147136/15. ;
XX
XX

XX New hybrid polypeptide, useful for preventing, treating and diagnosing
XX e.g. viral infections, comprises an enhancer peptide linked to a core
XX polypeptide.
XX
XX Disclosure; Page 58; 151pp; English.
XX
XX The present sequence is a core polypeptide which may be linked to an
XX enhancer peptide to form a novel hybrid polypeptide. The hybrid
XX polypeptide exhibits enhanced pharmacokinetic properties relative to
XX those exhibited by the core polypeptide when introduced into a living
XX system. It is used to increase the in vitro or ex vivo half-life of the
XX core polypeptide. The hybrid and core polypeptides can be used for
XX modulating fusogenic events and intracellular processes involving coiled-
XX coil peptide interactions. Other uses include preventing, treating and/or
XX diagnosing disorders involving fusion events (e.g. modulation of
XX neurotransmitter exchange and sperm-egg fusion), intracellular processes
XX involving coiled-coil peptides (e.g. bacterial infections) and viral
XX infections that involve cell-cell and/or virus-cell fusion (e.g. viral
XX infections caused by human immunodeficiency virus, respiratory syncytial
XX virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
XX polio virus). The enhancer peptide sequence increases the half-life and
XX reduces the clearance rate of therapeutic peptides, which increases their
XX efficacy and minimises the incidence and severity of adverse side
XX effects. In addition, this increases the sensitivity of the diagnostic
XX procedure in which they are used
XX
XX Sequence 36 AA;
XX
XX Query Match 100.0%; Score 36; DB 4; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 2e-27;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 YTGIIYNLLEESNQOEKNEQELLELDKRWANLWNWF 36
XX |||||||||||||||||||||||||||||||||||||||
XX 1 YTGIIYNLLEESNQOEKNEQELLELDKRWANLWNWF 36
XX
XX
XX RESULT 8
XX AAU70181
XX ID AAU70181 standard; peptide; 36 AA.
XX AC AAU70181;
XX DT 14-FEB-2002 (first entry)
XX DE HIV viral envelope protein stabilising peptide #3.
XX
XX Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;
XX anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
XX alpha-helical region; ectodomain.
XX
XX Homo sapiens.
XX
XX WO200170262-A2.
XX
XX 27-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-US008108.
XX
XX 17-MAR-2000; 2000US-0189981P.
XX
XX (PANA-) PANACOS PHARM INC.
XX
XX Wild CT, Allaway GP;
XX
XX WPI; 2001-626098/72.
XX
XX Immunogenic composition for inhibiting HIV infection, comprises viral
XX envelope protein or its fragment exterior to viral membrane, a
XX stabilizing peptide, and, optionally, viral cell surface receptor or its
XX fragment.
XX

PS Claim 6; Page 45; 84pp; English.

XX The invention relates to methods of generating immunogens that elicit neutralising antibodies which target regions of viral envelope proteins such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and AAU70677-AAU70743 represent stabilising peptides modelling the alpha-helical regions of the ectodomain of the HIV-1 transmembrane protein to stabilise fusion-active intermediate structures, which can be used as vaccine immunogens. Immunogenic compositions comprise a viral envelope protein or its fragment exterior to the viral membrane, a stabilising peptide to disrupt formation of structural intermediates necessary for viral fusion and entry, and optionally, a viral cell surface receptor or its fragment. The stabilising peptide is capable of associating with the envelope protein or its fragment to form a stabilised, fusion active structure. Antibody binding assays are used to determine the ability of immunogen vaccines to generate an immune response to various forms of envelope. Virus neutralisation assays can be used to characterise the antibody response raised against HIV-1 gp41 domains. The sequences and methods are useful for inhibiting HIV infection, for inducing an immune response in an animal and for raising antibodies

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQNOQKEQELLELDKWANLWNWF 36
|||||
DB 1 YTGIIYNLEESQNOQKEQELLELDKWANLWNWF 36
|||||

RESULT 9

ABB02832

ID ABB02832 standard; peptide; 36 AA.

XX AC ABB02832;

XX 11-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 03-JAN-2002 (first entry)

XX Viral core polypeptide, SEQ ID NO: 1359.

DE Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
KW infection.

OS Viruses.

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US003988.

PF 29-FEB-2000; 2000US-00515965.

PR (TRIM-) TRIMERIS INC.

PA Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
PT fusion, useful for treating HIV and Respiratory Syncytial Virus
PT infection.

XX Disclosure; Page 525; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)

CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQNOQKEQELLELDKWANLWNWF 36
|||||
DB 1 YTGIIYNLEESQNOQKEQELLELDKWANLWNWF 36
|||||

RESULT 10

ABB02831

ID ABB02831 standard; peptide; 36 AA.

XX AC ABB02831;

XX 11-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 03-JAN-2002 (first entry)

XX Viral core polypeptide, SEQ ID NO: 1358.

DE Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
KW infection.

OS Viruses.

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US003988.

PF 29-FEB-2000; 2000US-00515965.

PR (TRIM-) TRIMERIS INC.

PA Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
PT fusion, useful for treating HIV and Respiratory Syncytial Virus
PT infection.

XX Disclosure; Page 524-525; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)


```

DT 06-AUG-2003 (revised)
DT 03-JAN-2002 (first entry)
DE Viral DP178/107-like region peptide T1408.
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
KW infection.
XX Viruses.
OS WO200164013-A2.
PN XX
XX WO200164013-A2.
XX PD
XX 07-SEP-2001.
XX PF
XX 07-FEB-2001; 2001WO-US003988.
XX PR
XX 29-FEB-2000; 2000US-00515965.
XX PA (TRIM-) TRIMERIS INC.
XX PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX WPI; 2001-514829/56.
XX DR
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
PT fusion, useful for treating HIV and Respiratory Syncytial Virus
PT infection.
XX PS
XX Disclosure; Page 58; 587pp; English.
XX CC The invention relates to isolated analogues of the heptad repeat region
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
CC regions of proteins interact non-covalently with each other and/or with
CC peptides derived from them. This interaction is required for normal
CC infectivity of viruses such as RSV and HIV. The heptad repeat region
CC peptide analogues may be used to inhibit respiratory syncytial virus
CC (RSV) infection in a cell. They may also be used to inhibit HIV
CC infection. The present sequence is a peptide provided in the
CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
XX 11-SEP-2003 to standardise OS field)
XX SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36

RESULT 14
AAU13793
ID AAU13793 standard; peptide; 36 AA.
XX AC
XX AAU13793;
XX DT 21-NOV-2001 (first entry)
XX DE DP178-like/DP107-like peptide T-1408.
XX KW Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
XX antifusogenic; antiviral; HIV transmission; mutant; mutein.
XX OS Human immunodeficiency virus 1; isolate LAI.
XX OS Synthetic.
XX PN WO200151673-A2.
XX PD
XX 19-JUL-2001.

19-JUL-2001.
XX 05-JUL-2000; 2000WO-US035727.
XX 09-JUL-1999; 99US-00350841.
XX (TRIM-) TRIMERIS INC.
XX PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX PT Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.
XX PS
XX Disclosure; Page 77; 259pp; English.
XX CC The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents one of the DP178-like/DP107-like peptides of the invention
XX SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36

RESULT 15
AAU13792
ID AAU13792 standard; peptide; 36 AA.
XX AC
XX AAU13792;
XX DT 21-NOV-2001 (first entry)
XX DE DP178-like/DP107-like peptide T-1407.
XX KW Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
XX antifusogenic; antiviral; HIV transmission; mutant; mutein.
XX OS Human immunodeficiency virus 1; isolate LAI.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal is substituted by Ac"
FT Modified-site 36 /note= "C-terminal amide"
XX PN WO200151673-A2.
XX PD
XX 19-JUL-2001.

```


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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:19:28 ; Search time 19 Seconds
(without alignments)
182.305 Million cell updates/sec

Title: US-09-809-060A-3
Perfect score: 36
Sequence: 1 YGIIYNLESQKQKNEQLLELDKWNLNWNP 36

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	72.2	856	1 VCLJVL	env polyprotein pr
2	23	63.9	855	1 VCLJAJ	env polyprotein pr
3	21	58.3	357	2 S21994	envelope protein g
4	21	58.3	357	2 S21996	envelope protein g
5	21	58.3	443	2 C41621	env polyprotein p
6	21	58.3	847	2 T09448	envelope glycoprot
7	21	58.3	847	2 S13289	env protein - huma
8	21	58.3	851	2 S33985	env polyprotein -
9	21	58.3	854	2 S13288	env protein - huma
10	21	58.3	856	1 VCLJ3W	env polyprotein pr
11	21	58.3	856	1 VCLJH3	env polyprotein pr
12	21	58.3	861	1 VCLJSC	env polyprotein pr
13	21	58.3	861	1 VCLJLV	env polyprotein pr
14	19	52.8	357	2 S21992	envelope protein g
15	19	52.8	358	2 S21998	envelope protein g
16	16	44.4	853	2 S54384	env polyprotein
17	16	44.4	855	1 VCLJZR	env polyprotein pr
18	16	44.4	859	1 VCLJMN	env polyprotein pr
19	15	41.7	357	2 S22004	envelope protein g
20	15	41.7	357	2 S22006	envelope protein g
21	13	36.1	357	2 S21990	envelope protein g
22	13	36.1	843	1 H44001	env polyprotein pr
23	13	36.1	852	1 T12016	envelope glycoprot
24	12	33.3	358	2 S70417	envelope protein g
25	12	33.3	358	2 S22000	envelope protein g
26	12	33.3	358	2 S22002	envelope protein g
27	12	33.3	445	2 A41621	env polyprotein M
28	12	33.3	454	2 B41621	env polyprotein D
29	12	33.3	729	1 VCLJFK	env polyprotein pr

30 12 33.3 861 1 VCLJKB env polyprotein pr
31 11 30.6 856 1 A44963 env polyprotein pr
32 10 27.8 868 1 VCLJH4 env polyprotein -
33 9 25.0 846 1 VCLJND env polyprotein pr
34 9 25.0 852 1 VCLJBR -
35 9 25.0 859 2 T01672 envelope polyprote
36 8 22.2 592 2 T03682 catechol oxidase (
37 8 22.2 596 1 S33540 catechol oxidase (
38 8 22.2 599 2 T07097 catechol oxidase (
39 7 19.4 136 2 JU0266 envelope polyprote
40 7 19.4 136 2 JT0954 envelope polyprote
41 7 19.4 198 2 T46082 hypotetical prote
42 7 19.4 297 2 C90179 cysteine synthase
43 7 19.4 425 2 T19415 hypotetical prote
44 7 19.4 426 2 G69933 glutamate dehydrog
45 7 19.4 426 2 T01790 protoporphyrin IX

ALIGNMENTS

RESULT 1

VCLJVL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03974
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUE>
A:Cross-references: UNIPROT:P03376; UNIPARC:UPI000012A01F; GB:K02083; NID:G555008; PIDN:
C:Genetics:

RESULT 2

VCLJAJ
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03976
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Shi
Science 227, 484-492, 1985
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A:Reference number: A04003; MUID:85090453; PMID:2578227
A:Accession: A03976
A:Molecule type: DNA
A:Residues: 1-855 <SAN>
A:Cross-references: UNIPROT:P03378; UNIPARC:UPI000012A00F; GB:K02007; NID:G328658; PIDN:
C:Genetics:

Query Match 72.2%; Score 26; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 BESQKQKNEQLLELDKWNLNW 35
DB 647 BESQKQKNEQLLELDKWNLNW 672

```
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,150,184,190,200,244,265,292,304,334,341,358,364,388,394,400,408,445,458
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          53.9%; Score 23; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLEESQSQEKNEQELLELDKWA 30
DB 644 LLEESQSQEKNEQELLELDKWA 666

RESULT 3
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STEL>
A:Cross-references: UNIPROT:Q78118; UNIPARC:UPI0000178606; EMBL:X61355; NID:g60179; PIDN:R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STR2>
A:Cross-references: UNIPARC:UPI0000FF05F; EMBL:X61355; NID:g60179
C:Superfamily: type E retrovirus env polyprotein

Query Match          58.3%; Score 21; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 3.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQSQEKNEQELLELDKWA 30
DB 148 EESQSQEKNEQELLELDKWA 168

RESULT 4
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: UNIPROT:Q78119; UNIPARC:UPI0000104EC6; EMBL:X61356; NID:g60181; PIDN:A:Experimental source: patient 27L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match          58.3%; Score 21; DB 2; Length 357;
S13289
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```
Best Local Similarity 100.0%; Pred. No. 3.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQSQEKNEQELLELDKWA 30
DB 148 EESQSQEKNEQELLELDKWA 168

RESULT 5
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: UNIPROT:Q80023; UNIPARC:UPI0000104256; GB:M77230; NID:g328631; PIDN:A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: carboxyl end of coat protein gp41

Query Match          58.3%; Score 21; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQSQEKNEQELLELDKWA 30
DB 387 EESQSQEKNEQELLELDKWA 407

RESULT 6
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09448
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI000010C516; EMBL:U63632; NID:g1465777; PIDN:A:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match          58.3%; Score 21; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 8.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQSQEKNEQELLELDKWA 30
DB 638 EESQSQEKNEQELLELDKWA 658

RESULT 7
S13289
```

```
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13289
R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-847 <OR>
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI000017861B
C:Superfamily: type E retrovirus env polyprotein

Query Match 58.3%; Score 21; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 8.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWA 30
DB 638 EESQNOQEKNEQELLELDKWA 658

RESULT 8
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S33985
R/Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:Z11530; NID:g60192; PIDN
C:Superfamily: type E retrovirus env polyprotein

Query Match 58.3%; Score 21; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWA 30
DB 642 EESQNOQEKNEQELLELDKWA 662

RESULT 9
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C:Accession: S13288
R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OR>
A:Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:Q90178; UNIPROT:Q78243; UNIP
C:Superfamily: type E retrovirus env polyprotein

Query Match 58.3%; Score 21; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWA 30
DB 645 EESQNOQEKNEQELLELDKWA 665
```

RESULT 10
VCUJ3W

```
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: A24774
R/Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, B.S
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the env
A:Reference number: A24774; MUID:86218077; PMID:2423250
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: UNIPROT:P31872; UNIPARC:UPI000012A024; GB:K03455; GB:M38432; NID:g19
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,
```

```
Query Match 58.3%; Score 21; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 EESQNOQEKNEQELLELDKWA 30
DB 647 EESQNOQEKNEQELLELDKWA 667
```

RESULT 11
VCUJH3

```
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03973
R/Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran
Nberger, J.A.; Papas, T.S.; Graybe, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K0200
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,
```

```
Query Match 58.3%; Score 21; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 EESQNOQEKNEQELLELDKWA 30
DB 647 EESQNOQEKNEQELLELDKWA 667
```

RESULT 12
VCUJSC

```
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
```

N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C;Accession: B28922
R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staal, A.; Weiss, R.A.; Gallo, R.C. J. Virol. 64, 531-536, 1988
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
A;Accession: B28922
A;Molecule type: DNA
A;Residues: 1-861 <GUR>
A;Cross-references: UNIPARC:UPI0000174A39
C;Genetics: env
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-861/Product: env polyprotein #status predicted <EP>
F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 58.3%; Score 21; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 9.1e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30
|||||
Db 652 EESQOQEKNEQELLELDKWA 672

RESULT 13
VCILJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03975
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M. Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <WAI>
A;Cross-references: UNIPROT:P03377; UNIPARC:UPI000012A013; GB:K02013; NID:G326417; PIDN: C;Genetics: env
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F;517-861/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,617,618,619,620,621,622,623,624,625,626,627,628,629,630,631,632,633,634,635,636,637,638,639,640,641,642,643,644,645,646,647,648,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,664,665,666,667,668,669,670,671,672,673,674,675,676,677,678,679,680,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000,1001,1002,1003,1004,1005,1006,1007,1008,1009,1010,1011,1012,1013,1014,1015,1016,1017,1018,1019,1020,1021,1022,1023,1024,1025,1026,1027,1028,1029,1030,1031,1032,1033,1034,1035,1036,1037,1038,1039,1040,1041,1042,1043,1044,1045,1046,1047,1048,1049,1050,1051,1052,1053,1054,1055,1056,1057,1058,1059,1060,1061,1062,1063,1064,1065,1066,1067,1068,1069,1070,1071,1072,1073,1074,1075,1076,1077,1078,1079,1080,1081,1082,1083,1084,1085,1086,1087,1088,1089,1090,1091,1092,1093,1094,1095,1096,1097,1098,1099,1100,1101,1102,1103,1104,1105,1106,1107,1108,1109,1110,1111,1112,1113,1114,1115,1116,1117,1118,1119,1120,1121,1122,1123,1124,1125,1126,1127,1128,1129,1130,1131,1132,1133,1134,1135,1136,1137,1138,1139,1140,1141,1142,1143,1144,1145,1146,1147,1148,1149,1150,1151,1152,1153,1154,1155,1156,1157,1158,1159,1160,1161,1162,1163,1164,1165,1166,1167,1168,1169,1170,1171,1172,1173,1174,1175,1176,1177,1178,1179,1180,1181,1182,1183,1184,1185,1186,1187,1188,1189,1190,1191,1192,1193,1194,1195,1196,1197,1198,1199,1200,1201,1202,1203,1204,1205,1206,1207,1208,1209,1210,1211,1212,1213,1214,1215,1216,1217,1218,1219,1220,1221,1222,1223,1224,1225,1226,1227,1228,1229,1230,1231,1232,1233,1234,1235,1236,1237,1238,1239,1240,1241,1242,1243,1244,1245,1246,1247,1248,1249,1250,1251,1252,1253,1254,1255,1256,1257,1258,1259,1260,1261,1262,1263,1264,1265,1266,1267,1268,1269,1270,1271,1272,1273,1274,1275,1276,1277,1278,1279,1280,1281,1282,1283,1284,1285,1286,1287,1288,1289,1290,1291,1292,1293,1294,1295,1296,1297,1298,1299,1300,1301,1302,1303,1304,1305,1306,1307,1308,1309,1310,1311,1312,1313,1314,1315,1316,1317,1318,1319,1320,1321,1322,1323,1324,1325,1326,1327,1328,1329,1330,1331,1332,1333,1334,1335,1336,1337,1338,1339,1340,1341,1342,1343,1344,1345,1346,1347,1348,1349,1350,1351,1352,1353,1354,1355,1356,1357,1358,1359,1360,1361,1362,1363,1364,1365,1366,1367,1368,1369,1370,1371,1372,1373,1374,1375,1376,1377,1378,1379,1380,1381,1382,1383,1384,1385,1386,1387,1388,1389,1390,1391,1392,1393,1394,1395,1396,1397,1398,1399,1400,1401,1402,1403,1404,1405,1406,1407,1408,1409,1410,1411,1412,1413,1414,1415,1416,1417,1418,1419,1420,1421,1422,1423,1424,1425,1426,1427,1428,1429,1430,1431,1432,1433,1434,1435,1436,1437,1438,1439,1440,1441,1442,1443,1444,1445,1446,1447,1448,1449,1450,1451,1452,1453,1454,1455,1456,1457,1458,1459,1460,1461,1462,1463,1464,1465,1466,1467,1468,1469,1470,1471,1472,1473,1474,1475,1476,1477,1478,1479,1480,1481,1482,1483,1484,1485,1486,1487,1488,1489,1490,1491,1492,1493,1494,1495,1496,1497,1498,1499,1500,1501,1502,1503,1504,1505,1506,1507,1508,1509,1510,1511,1512,15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FT CARBOHYD 254 254 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 275 275 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 289 289 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 302 302 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 308 308 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 314 314 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 344 344 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 351 351 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 367 367 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 397 397 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 403 403 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 407 407 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 413 413 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 418 418 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 455 455 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 471 471 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 620 620 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 625 625 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 634 634 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 646 646 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 825 825 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 53 73 By similarity.
FT DISULFID 118 218 By similarity.
FT DISULFID 125 209 By similarity.
FT DISULFID 130 157 By similarity.
FT DISULFID 231 260 By similarity.
FT DISULFID 241 252 By similarity.
FT DISULFID 309 343 By similarity.
FT DISULFID 389 452 By similarity.
FT DISULFID 396 425 By similarity.
SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;

Query Match 100.0%; Score 36; DB 1; Length 865;
Best Local Similarity 100.0%; Pred. No. 2.9e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQOQKNEQELLELDKQWNLWNWF 36
Db 647 YTGIIYNLEESQOQKNEQELLELDKQWNLWNWF 682

RESULT 2
Q90DJ7_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q90DJ7_9HIV1 PRELIMINARY; PRT; 122 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UG;
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempaia S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307734; AAL08795.1; -; Genomic_DNA.
DR HSSP; P04624; 1JAU.
DR SMR; Q90DJ7; 1-105.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14743 MW; FBB3D55A1B1482A2 CRC64;

Query Match 91.7%; Score 33; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.9e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IYNLEESQOQKNEQELLELDKQWNLWNWF 36
Db 81 IYNLEESQOQKNEQELLELDKQWNLWNWF 113

RESULT 3
Q4VUS2_9HIV1 PRELIMINARY; PRT; 120 AA.
AC Q4VUS2_9HIV1 PRELIMINARY; PRT; 120 AA.
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M12;
RA Santos A.L., Martinez A.M.B., Sassi R.M., D'Hora V., Soares E.A.J.M.,
RA D'Avila N., Silveira J., Mendonca V.S., Leal R.G., Tanuri A.,
RA Soares M.A.;
RT "Determinants of HIV-1 Mother-to-Child Transmission in Southern Brazil."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY621387; AAW47844.1; -; Genomic_DNA.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 14330 MW; BEF6E3214CB8D65 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.6e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLEESQOQKNEQELLELDKQWNLWNWF 36
Db 82 IYNLEESQOQKNEQELLELDKQWNLWNWF 113

RESULT 4
Q6WH26_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q6WH26_9HIV1 PRELIMINARY; PRT; 122 AA.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14715797; DOI=10.1128/JCM.42.1.426-430.2004;
RA Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,
RA Gouvea M.I.F.S., Guimaraes M.A.M., De Oliveira F.E.,
RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;
RT "Prevalence of human immunodeficiency virus drug resistance mutations and subtypes in drug-naive, infected individuals in the army health service of Rio de Janeiro, Brazil."
RL J. Clin. Microbiol. 42:426-430(2004).
DR EMBL; AY285070; AAQ68133.1; -; Genomic_RNA.
DR SMR; Q6WH26; 1-105.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.

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DR GO: 0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14758 MW; B2F2785E75F8427E CRC64;

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.6e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQKNEQELLELDKQANLWNWF 36
DB 82 IYNLLEESQOQKNEQELLELDKQANLWNWF 113

RESULT 5
OQIWI9_9HIV1
ID OQIWI9_9HIV1 PRELIMINARY; PRT; 122 AA.
AC OQIWI9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21580799; PubMed=11724274; DOI=10.1023/A:1011812810397;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer-Silva W.A., Sion F.S., Passioni L.F.C.,
RA Menezes J.A., Calazans A.R., Tanuri A.;
RT "Genotypic and phenotypic evidence of different drug-resistance
RT mutation patterns between B and non-B subtype isolates of human
RT immunodeficiency virus type 1 found in Brazilian patients failing
RT HAART.";
RL Virus Genes 23:193-202 (2001).
DR EMBL: AF165535; AAF08480.1; -; Genomic_DNA.
DR HSSP: FI2488; IIM7.
DR SMR; QOQIWI9; 1-105.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0019031; C: viral envelope; IEA.
DR GO: 0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14744 MW; 02F0BE9F79AE6C75 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.6e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQKNEQELLELDKQANLWNWF 36
DB 82 IYNLLEESQOQKNEQELLELDKQANLWNWF 113

RESULT 6
Q53I38_9HIV1
ID Q53I38_9HIV1 PRELIMINARY; PRT; 143 AA.
AC Q53I38;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=gp41;
OS Human immunodeficiency virus 1.
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OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15328081; DOI=10.1128/AAC.48.9.3253-3259.2004;
RA Menzo S., Castagna A., Monchetti A., Hasson H., Danise A., Carini E.,
RA Bagnarelli P., Lazzarin A., Clementi M.;
RT "Genotype and phenotype patterns of human immunodeficiency virus type
RT 1 resistance to enfuvirtide during long-term treatment.";
RL Antimicrob. Agents Chemother. 48:3253-3259 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Menzo S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ964909; CAI79657.1; -; Genomic_RNA.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 143
FT NON_TER 143
SQ SEQUENCE 143 AA; 16814 MW; 86046F46914618F9 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 4.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IYNLLEESQOQKNEQELLELDKQANLWNWF 35
DB 112 IYNLLEESQOQKNEQELLELDKQANLWNWF 143

RESULT 7
Q6UYPJ_9HIV1
ID Q6UYPJ_9HIV1 PRELIMINARY; PRT; 848 AA.
AC Q6UYPJ;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstan K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Molinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807 (2004).
DR EMBL: AY357545; AAR00902.1; -; Genomic_DNA.
DR HSSP: PD4578; IK33.
DR SMR; Q6UYPJ; 82-126, 194-490, 538-624.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0019031; C: viral envelope; IEA.
DR GO: 0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 848 AA; 96698 MW; 50341627DE7FB6BA CRC64;

Query Match 88.9%; Score 32; DB 2; Length 848;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQKNEQELLELDKQANLWNWF 36
DB 640 IYNLLEESQOQKNEQELLELDKQANLWNWF 671
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 848 AA; 96636 MW; 6077A991B48B1403 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 848;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQEKNEQELLELDKQANLWNWF 36
Db 640 IYNLLEESQOQEKNEQELLELDKQANLWNWF 671

RESULT 10
Q6UYP7_9HIV1
ID Q6UYP7_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYP7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357544; AAR00901.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYP4; 194-490, 538-624.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 848 AA; 96634 MW; CD041E0BAC44DB3B CRC64;

Query Match 88.9%; Score 32; DB 2; Length 848;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQEKNEQELLELDKQANLWNWF 36
Db 640 IYNLLEESQOQEKNEQELLELDKQANLWNWF 671

RESULT 9
Q6UYP5_9HIV1
ID Q6UYP5_9HIV1 PRELIMINARY; PRT; 848 AA.
AC Q6UYP5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357543; AAR00900.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYP5; 194-490, 538-624.
DR GO; GO:0016021; C:integral to membrane; IEA.

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQEKNEQELLELDKQANLWNWF 36
Db 641 IYNLLEESQOQEKNEQELLELDKQANLWNWF 672

RESULT 11
Q6UYP8_9HIV1
ID Q6UYP8_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYP8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
```



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OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL: AY357538; AAR00897.1; -; Genomic_DNA.
DR HSSP: P04578; IK33.
DR SMR: Q6UYQ3; 1-206, 194-491, 539-625.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 849 AA; 96654 MW; DB9F480D9A9D14F9 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 641 IYNLEESQOQEKNEQELLELDKQWNLWNWF 672

RESULT 12
Q6UYQ3_9HIV1
ID Q6UYQ3_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYQ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL: AY357538; AAR00897.1; -; Genomic_DNA.
DR HSSP: P04578; IK33.
DR SMR: Q6UYQ3; 1-217, 194-490, 535-624.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 849 AA; 96637 MW; A30D2A6F412F19A9 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 640 IYNLEESQOQEKNEQELLELDKQWNLWNWF 671

RESULT 14
Q6UYQ5_9HIV1
ID Q6UYQ5_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYQ5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL: AY357537; AAR00896.1; -; Genomic_DNA.
DR HSSP: P04578; IK33.
DR SMR: Q6UYQ9; 194-491, 539-625.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 849 AA; 96663 MW; BCBD828AB942F2E CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 641 IYNLEESQOQEKNEQELLELDKQWNLWNWF 672

RESULT 13
Q6UYQ3_9HIV1
ID Q6UYQ3_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYQ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL: AY357533; AAR00892.1; -; Genomic_DNA.
DR HSSP: P04578; IK33.
DR SMR: Q6UYQ3; 1-217, 194-490, 535-624.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 849 AA; 96637 MW; A30D2A6F412F19A9 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 640 IYNLEESQOQEKNEQELLELDKQWNLWNWF 671

RESULT 14
Q6UYQ5_9HIV1
ID Q6UYQ5_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYQ5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL: AY357537; AAR00896.1; -; Genomic_DNA.
DR HSSP: P04578; IK33.
DR SMR: Q6UYQ9; 194-491, 539-625.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 849 AA; 96663 MW; BCBD828AB942F2E CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357530; AAR00890.1; -; Genomic_DNA.
DR HSSP; P04578; IK33.
DR SMR; Q6UYQ5; 194-490, 535-624.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF0516; GP120; 1.
DR Pfam; PF0517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 849 AA; 96667 MW; CED40F4AE1574B58 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQEKNEQELLELDKQANLWNWF 36
   |||||
Db 640 IYNLLEESQOQEKNEQELLELDKQANLWNWF 671

RESULT 15
Q6UYQ6_9HIV1
ID Q6UYQ6_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYQ6_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14950699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357529; AAR00889.1; -; Genomic_DNA.
DR HSSP; P04578; IK33.
DR SMR; Q6UYQ6; 194-490, 538-624.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF0516; GP120; 1.
DR Pfam; PF0517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 849 AA; 96782 MW; 8061276D3343029A CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQEKNEQELLELDKQANLWNWF 36
   |||||
Db 640 IYNLLEESQOQEKNEQELLELDKQANLWNWF 671
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Search completed: March 6, 2006, 15:25:17
Job time : 123 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 16:25:38 ; Search time 28.6667 Seconds
(without alignments)
103.825 Million cell updates/sec

Title: US-09-809-060A-3
Perfect score: 36
Sequence: 1 YTGIIYNLEESQKQKNEQELLELDKWNLNWVF 36

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	36	1	US-08-073-028-4
2	36	100.0	36	2	US-08-486-099-4
3	36	100.0	36	2	US-08-360-107A-4
4	36	100.0	36	2	US-08-484-223B-4
5	36	100.0	36	2	US-08-919-597-4
6	36	100.0	36	2	US-08-475-668A-4
7	36	100.0	36	2	US-08-485-551A-4
8	36	100.0	36	2	US-08-471-913A-4
9	36	100.0	36	2	US-08-554-616-4
10	36	100.0	36	2	US-08-485-264A-4
11	36	100.0	36	2	US-09-082-279B-1358
12	36	100.0	36	2	US-09-082-279B-1359
13	36	100.0	36	2	US-08-474-349A-4
14	36	100.0	36	2	US-09-315-304B-1358
15	36	100.0	36	2	US-09-315-304B-1359
16	36	100.0	36	2	US-08-255-208A-4
17	36	100.0	36	2	US-08-973-952-4
18	36	100.0	36	2	US-08-470-896-4
19	36	100.0	36	2	US-08-485-546A-4
20	36	100.0	36	2	US-09-834-784-1358
21	36	100.0	36	2	US-09-834-784-1359
22	36	100.0	36	2	US-09-515-965A-1358
23	36	100.0	36	2	US-09-515-965A-1359
24	36	100.0	36	2	US-09-350-641C-1358
25	36	100.0	36	2	US-09-350-641C-1359
26	36	100.0	36	2	US-09-350-841A-1358
27	36	100.0	36	2	US-09-350-841A-1359

28	36	100.0	36	2	US-08-487-266A-4	Sequence 4, Appli
29	36	100.0	36	2	US-09-623-548A-1422	Sequence 1422, Ap
30	36	100.0	36	2	US-10-252-136-4	Sequence 4, Appli
31	36	100.0	36	2	US-09-657-276-1422	Sequence 1422, Ap
32	36	100.0	36	2	US-08-484-741-4	Sequence 4, Appli
33	36	100.0	138	2	US-09-570-921-18	Sequence 18, Appli
34	36	100.0	269	2	US-08-965-056-33	Sequence 33, Appli
35	36	100.0	865	2	US-07-956-483-13	Sequence 13, Appli
36	36	100.0	887	2	US-08-472-240A-4	Sequence 4, Appli
37	26	72.2	36	1	US-08-073-028-3	Sequence 3, Appli
38	26	72.2	36	2	US-08-360-107A-3	Sequence 3, Appli
39	26	72.2	36	2	US-08-554-616-3	Sequence 3, Appli
40	26	72.2	36	2	US-09-350-841A-1543	Sequence 1543, Ap
41	26	72.2	138	2	US-09-570-921-23	Sequence 23, Appli
42	23	63.9	36	2	US-08-486-099-3	Sequence 3, Appli
43	23	63.9	36	2	US-08-484-223B-3	Sequence 3, Appli
44	23	63.9	36	2	US-08-919-597-3	Sequence 3, Appli
45	23	63.9	36	2	US-08-475-668A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-073-028-4
; Sequence 4, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-073-028-4

Query Match 100.0%; Score 36; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQKQKNEQELLELDKWNLNWVF 36
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Db 1 YTGIIYNLLEESQKNEQKNEQELLELDKQWNLWNWF 36

RESULT 2

US-08-486-099-4

; Sequence 4, Application US/08486099

; Patent No. 6013263

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

; NUMBER OF SEQUENCES: 209

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,099

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-486-099-4

Query Match 100.0%; Score 36; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-27;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQKNEQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQKNEQELLELDKQWNLWNWF 36

RESULT 3

US-08-360-107A-4

; Sequence 4, Application US/08360107A

; Patent No. 6017536

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

; NUMBER OF SEQUENCES: 149

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/360,107A

; FILING DATE: 20-DEC-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-013

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-360-107A-4

Query Match 100.0%; Score 36; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-27;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQKNEQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQKNEQELLELDKQWNLWNWF 36

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 5

US-08-919-597-4
Sequence 4, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864.

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6

US-08-475-668A-4
Sequence 4, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

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RESULT 7
US-08-485-551A-4
; Sequence 4, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-485-551A-4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. NO. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36

RESULT 8
US-08-471-913A-4
; Sequence 4, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
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; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-471-913A-4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. NO. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36

RESULT 9
US-08-554-616-4
; Sequence 4, Application US/08554616
; Patent No. 6133418
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,616
; FILING DATE: 06-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER: US 08/073,028
; FILING DATE: 07-JUN-1993
```

ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-554-616-4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 11
US-09-082-279B-1358
; Sequence 1358, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1358
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-1358

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 12
US-09-082-279B-1359
; Sequence 1359, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1359
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-1359

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-554-616-4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 10
US-08-485-264A-4
; Sequence 4, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNWF 36
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNWF 36

RESULT 13

US-08-474-349A-4
; Sequence 4, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNWF 36
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNWF 36

RESULT 14

US-09-315-304B-1358
; Sequence 1358, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.

; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1358
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1358

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNWF 36
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNWF 36

RESULT 15

US-09-315-304B-1359
; Sequence 1359, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1359
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1359

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNWF 36
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNWF 36

Search completed: March 6, 2006, 16:27:50
Job time : 28.6667 secs

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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:26:33 ; Search time 97.3333 Seconds
(without alignments)
154.540 Million cell updates/sec

Title: US-09-809-060A-3
Perfect score: 36
Sequence: 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36

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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	36	3	US-09-809-060-3
2	36	100.0	36	4	US-10-252-136-4
3	36	100.0	36	4	US-10-351-641-1358
4	36	100.0	36	4	US-10-351-641-1359
5	36	100.0	36	4	US-10-267-682-4
6	36	100.0	36	4	US-10-267-748-4
7	36	100.0	36	4	US-10-663-589-39
8	36	100.0	36	4	US-10-671-282-39
9	36	100.0	36	5	US-10-168-295-4
10	36	100.0	36	5	US-10-950-010-4
11	36	100.0	36	6	US-11-066-697-1422
12	36	100.0	269	3	US-09-854-816-33
13	26	72.2	38	4	US-10-086-409A-3
14	26	72.2	45	4	US-10-086-409A-6
15	23	63.9	36	3	US-09-809-060-2
16	23	63.9	36	4	US-10-252-136-3
17	23	63.9	36	4	US-10-351-641-856
18	23	63.9	36	4	US-10-351-641-1051
19	23	63.9	36	4	US-10-351-641-1357
20	23	63.9	36	4	US-10-267-682-3
21	23	63.9	36	4	US-10-267-748-3
22	23	63.9	36	4	US-10-663-589-38
23	23	63.9	36	4	US-10-671-282-38
24	23	63.9	36	5	US-10-168-295-3
25	23	63.9	36	5	US-10-950-010-3
26	23	63.9	36	5	US-10-950-010-541
27	23	63.9	36	6	US-11-066-697-1421

28 23 63.9 70 6 US-11-018-102-13 Sequence 13, Appl
29 23 63.9 145 3 US-09-131-551-11 Sequence 11, Appl
30 23 63.9 145 4 US-10-000-321-11 Sequence 11, Appl
31 23 63.9 269 3 US-09-854-816-28 Sequence 28, Appl
32 23 63.9 269 3 US-09-854-816-30 Sequence 30, Appl
33 23 63.9 269 3 US-09-854-816-31 Sequence 31, Appl
34 23 63.9 285 6 US-11-018-102-11 Sequence 11, Appl
35 21 58.3 21 4 US-10-351-641-1082 Sequence 1082, Ap
36 21 58.3 21 4 US-10-351-641-1083 Sequence 1083, Ap
37 21 58.3 27 4 US-10-005-305-58 Sequence 58, Appl
38 21 58.3 27 5 US-10-005-305-73 Sequence 73, Appl
39 21 58.3 27 5 US-10-950-010-125 Sequence 125, App
40 21 58.3 28 4 US-10-005-305-59 Sequence 59, Appl
41 21 58.3 28 4 US-10-005-305-72 Sequence 72, Appl
42 21 58.3 28 5 US-10-950-010-124 Sequence 124, App
43 21 58.3 29 4 US-10-351-641-635 Sequence 635, App
44 21 58.3 29 4 US-10-351-641-637 Sequence 637, App
45 21 58.3 29 4 US-10-005-305-60 Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-09-809-060-3
; Sequence 3, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; TITLE OF INVENTION: Regions of HIV Envelope Proteins
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-3

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 98-28; 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36

RESULT 2

US-10-252-136-4
; Sequence 4, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

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/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Human immunodeficiency virus
US-10-252-136-4

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKWANLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKWANLWNWF 36

RESULT 3
US-10-351-641-1358
/ Sequence 1358, Application US/10351641
/ Publication No. US20030186874A1
/ GENERAL INFORMATION:
/ APPLICANT: Barney, S.
/ APPLICANT: Guthrie, K.
/ APPLICANT: Merutka, G.
/ APPLICANT: Anwer, M.
/ APPLICANT: Lambert, D.
/ TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
/ FILE REFERENCE: 7872-100
/ CURRENT APPLICATION NUMBER: US/10/351,641
/ CURRENT FILING DATE: 2003-01-24
/ PRIOR APPLICATION NUMBER: 09/350,641
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: 09/315,304
/ PRIOR FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: 09/082,279
/ PRIOR FILING DATE: 1998-05-20
/ NUMBER OF SEQ ID NOS: 1757
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1358
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Core polypeptide
US-10-351-641-1358

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKWANLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKWANLWNWF 36

RESULT 4
US-10-351-641-1359
/ Sequence 1359, Application US/10351641
/ Publication No. US20030186874A1
/ GENERAL INFORMATION:
/ APPLICANT: Barney, S.
/ APPLICANT: Guthrie, K.
/ APPLICANT: Merutka, G.
/ APPLICANT: Anwer, M.
/ APPLICANT: Lambert, D.
/ TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
/ FILE REFERENCE: 7872-100
/ CURRENT APPLICATION NUMBER: US/10/351,641
/ CURRENT FILING DATE: 2003-01-24
/ PRIOR APPLICATION NUMBER: 09/350,641
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: 09/315,304
/ PRIOR FILING DATE: 1998-05-20
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/ PRIOR APPLICATION NUMBER: 09/082,279
/ PRIOR FILING DATE: 1998-05-20
/ NUMBER OF SEQ ID NOS: 1757
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1359
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Core polypeptide
US-10-351-641-1359

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKWANLWNWF 36
Db 1 YTGIIYNLLEESQKQKNEQELLELDKWANLWNWF 36

RESULT 5
US-10-267-682-4
/ Sequence 4, Application US/10267682
/ Publication No. US20040033235A1
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ APPLICANT: Matthews, Thomas J.
/ APPLICANT: Wild, Carl T.
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ APPLICANT: Langlois, Alphonse J.
/ TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
/ MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
/ TRANSMISSION
/ NUMBER OF SEQUENCES: 239
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA: US/10/267,682
/ APPLICATION NUMBER: US/10/267,682
/ FILING DATE: 08-Oct-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,223A
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-029
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-267-682-4
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Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36

RESULT 6
US-10-267-748-4
; Sequence 4, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-267-748-4

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36

RESULT 7

US-10-663-589-39
; Sequence 39, Application US/10663589
; Publication No. US20040063637A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; peptide
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 39
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-39

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36

RESULT 8
US-10-671-282-39
; Sequence 39, Application US/10671282
; Publication No. US20040122214A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
; their use in therapy
; FILE REFERENCE: TRM-004
; CURRENT APPLICATION NUMBER: US/10/671,282
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/414,439
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 39
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-671-282-39

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQNOQKNEQELLELDKQWNLWNWF 36

RESULT 9
US-10-168-295-4
; Sequence 4, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Baroudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19

RESULT 11
US-11-066-697-1422
; Sequence 1422, Application US/11066697
; Publication NO. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Karen L.

RESULT 12
US-09-854-816-33
; Sequence 33, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovasnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881

```

: APPLICANT: Hunt, Jeffrey C.
: APPLICANT: Dawson, George J.
: APPLICANT: Sarin, Virender K.
: APPLICANT: Webber, J. Scott
: APPLICANT: Wray, Larry K.
: APPLICANT: Falk, Lawrence A.
: APPLICANT: Devare, Sushil G.
: TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODY (5-21-3) TO
: TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS gp41 PROTEIN
: FILE REFERENCE: 4573.US.C6
: CURRENT APPLICATION NUMBER: US/10/086,409A
: CURRENT FILING DATE: 2001-11-19
: PRIOR APPLICATION NUMBER: 08/856,155
: PRIOR FILING DATE: 1997-05-14
: PRIOR APPLICATION NUMBER: 08/579,088
: PRIOR FILING DATE: 1995-12-27
: PRIOR APPLICATION NUMBER: 08/376,694
: PRIOR FILING DATE: 1995-01-23
: PRIOR APPLICATION NUMBER: 08/101,082
: PRIOR FILING DATE: 1993-08-02
: PRIOR APPLICATION NUMBER: 07/780,576
: PRIOR FILING DATE: 1991-10-22
: PRIOR APPLICATION NUMBER: 07/176,077
: PRIOR FILING DATE: 1988-03-30
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 45
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Peptide corresponding to gp41 amino
: OTHER INFORMATION: acids 131 - 175
US-10-086-409A-6

Query Match 72.2%; Score 26; DB 4; Length 45;
Best Local Similarity 100.0%; Pred.No. 5.7e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

Qy 10 EESNQOEKNEQELLELDKWLNNW 35
Db 6 EESNQOEKNEQELLELDKWLNNW 31

RESULT 15
US-09-809-060-2
: Sequence 2, Application US/09809060
: Publication No. US20020010317A1
: GENERAL INFORMATION:
: APPLICANT: Wild, Carl T.
: APPLICANT: Alloway, Graham P.
: TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
: TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
: TITLE OF INVENTION: Regions of HIV Envelope Proteins
: FILE REFERENCE: 1900.026001
: CURRENT APPLICATION NUMBER: US/09/809,060
: CURRENT FILING DATE: 2001-03-16
: PRIOR APPLICATION NUMBER: US 60/189,981
: PRIOR FILING DATE: 2000-03-17
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 2
: LENGTH: 36
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-2

Query Match 63.9%; Score 23; DB 3; Length 36;
Best Local Similarity 100.0%; Pred.No. 3.8e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0;

Qy 8 LLEESNQOEKNEQELLELDKWA 30

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Db 8 LLEESQOQEKNEQELLELDKWA 30

Search completed: March 6, 2006, 16:32:48
Job time : 97.3333 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:28:08 ; Search time 10.3333 Seconds
(without alignments)
69.679 Million cell updates/sec

Title: US-09-809-060A-3
Perfect score: 36
Sequence: 1 YTGIIYNLLSESQKQKNEQELLELDKWNLWHP 36

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 135346 seqs, 20000420 residues

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Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Published Applications AA New.*
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3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
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6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	63.9	145	7	US-11-084-858-11
2	21	58.3	36	6	US-10-841-956A-1
3	21	58.3	36	7	US-11-029-003-1
4	21	58.3	36	7	US-11-187-687-22
5	21	58.3	37	7	US-11-112-277-33
6	21	58.3	44	7	US-11-089-426-10
7	21	58.3	44	7	US-11-187-687-24
8	21	58.3	267	6	US-10-841-956A-4
9	21	58.3	269	6	US-10-841-956A-8
10	21	58.3	270	6	US-10-841-956A-5
11	21	58.3	281	6	US-10-841-956A-7
12	21	58.3	282	6	US-10-841-956A-6
13	21	58.3	293	6	US-10-841-956A-9
14	21	58.3	354	7	US-11-053-100-27
15	21	58.3	356	7	US-11-053-100-36
16	21	58.3	357	7	US-11-053-100-30
17	21	58.3	357	7	US-11-053-100-33
18	21	58.3	504	7	US-11-053-100-28
19	21	58.3	506	7	US-11-053-100-37
20	21	58.3	507	7	US-11-053-100-31
21	21	58.3	507	7	US-11-053-100-34
22	21	58.3	654	7	US-11-053-100-29
23	21	58.3	656	7	US-11-053-100-38
24	21	58.3	657	7	US-11-053-100-32
25	21	58.3	657	7	US-11-053-100-35

RESULT 1
US-11-084-858-11
; Sequence 11, Application US/11084858
; Publication No. US20050271678A1
; GENERAL INFORMATION:
; APPLICANT: KRUST, Stefan
; KNAPP, Stefan
; GERKEN, Manfred
; GUERTLER, Lutz
; TITLE OF INVENTION: Peptides derived from a retrovirus of
; the HIV group, and their use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/084,858
; FILING DATE: 21-Mar-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/000,321
; FILING DATE: 04-Dec-2001
; APPLICATION NUMBER: 09/131,551
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 58315/106/BEAK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ALIGNMENTS

26 21 58.3 856 6 US-10-510-947-8 Sequence 8, Appli
27 21 58.3 856 7 US-11-042-988-13 Sequence 13, Appli
28 21 58.3 856 7 US-11-135-235-1 Sequence 1, Appli
29 19 52.8 36 6 US-10-506-796A-5 Sequence 5, Appli
30 16 44.4 35 6 US-10-506-796A-1 Sequence 1, Appli
31 16 44.4 36 6 US-10-506-796A-3 Sequence 3, Appli
32 16 44.4 38 7 US-11-151-598-4 Sequence 4, Appli
33 16 44.4 171 6 US-10-506-796A-9 Sequence 9, Appli
34 16 44.4 213 6 US-10-841-956A-19 Sequence 19, Appli
35 16 44.4 220 7 US-11-151-598-1 Sequence 1, Appli
36 16 44.4 225 7 US-11-151-598-8 Sequence 7, Appli
37 16 44.4 225 7 US-11-151-598-7 Sequence 7, Appli
38 16 44.4 227 7 US-11-151-598-9 Sequence 9, Appli
39 16 44.4 267 7 US-11-151-598-2 Sequence 2, Appli
40 15 41.7 34 7 US-11-112-277-6 Sequence 6, Appli
41 15 41.7 34 7 US-11-112-277-6 Sequence 6, Appli
42 15 41.7 34 7 US-11-112-277-36 Sequence 36, Appli
43 15 41.7 34 7 US-11-112-277-38 Sequence 38, Appli
44 15 41.7 34 7 US-11-151-598-10 Sequence 10, Appli
45 15 41.7 34 7 US-11-151-598-12 Sequence 12, Appli

US-11-084-858-11

Query Match 63.9%; Score 23; DB 7; Length 145;
Best Local Similarity 100.0%; Pred. No. 9.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLEESQKQKNEQELLELDKWA 30
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DB 113 LLEESQKQKNEQELLELDKWA 135

RESULT 2

US-10-841-956A-1
; Sequence 1, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-1

Query Match 58.3%; Score 21; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKQKNEQELLELDKWA 30
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DB 10 EESQKQKNEQELLELDKWA 30

RESULT 3

US-11-029-003-1
; Sequence 1, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEL, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029,003
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539,207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487,964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469,600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-029-003-1

Query Match 58.3%; Score 21; DB 7; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKQKNEQELLELDKWA 30
|||||
DB 10 EESQKQKNEQELLELDKWA 30

RESULT 4

US-11-187-687-22
; Sequence 22, Application US/11187687
; Publication No. US20060019347A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Ho Sung
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Hays, Anna-Maria
; APPLICANT: Wilson, Troy E.
; APPLICANT: Litzinger, David C.
; APPLICANT: Mariani, Roberto
; APPLICANT: Kimmel, Bruce E.
; APPLICANT: Keefe, William M.
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
; FILE REFERENCE: AMEX-0041.00US
; CURRENT APPLICATION NUMBER: US/11/187,687
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: 60/590,035
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: 60/659,709
; PRIOR FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-22

Query Match 58.3%; Score 21; DB 7; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKQKNEQELLELDKWA 30
|||||
DB 10 EESQKQKNEQELLELDKWA 30

RESULT 5

US-11-112-277-33
; Sequence 33, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T20 Analogue
; FEATURE:
; NAME/KEY: MOD_RES


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; LOCATION: 37
; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-33

Query Match      58.3%; Score 21; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30
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Db 10 EESQOQEKNEQELLELDKWA 30

RESULT 6
US-11-089-426-10
; Sequence 10, Application US/11089426
; Publication No. US20050261229A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: Fc Fusion Proteins For Enhancing the Immunogenicity of
; FILE REFERENCE: LEX-007
; CURRENT APPLICATION NUMBER: US/11/089,426
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US/09/621,268
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/144,965
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fused
; OTHER INFORMATION: polypeptide from pDC-muFC vector
US-11-089-426-10

Query Match      58.3%; Score 21; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.3e-15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30
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Db 8 EESQOQEKNEQELLELDKWA 28

RESULT 7
US-11-187-687-24
; Sequence 24, Application US/11187687
; Publication No. US20060019347A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Ho Sung
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Hays, Anna-Maria
; APPLICANT: Wilson, Troy E.
; APPLICANT: Litzynger, David C.
; APPLICANT: Mariani, Roberto
; APPLICANT: Kimmel, Bruce E.
; APPLICANT: Keefe, William M.
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
; FILE REFERENCE: AMBX-0041.00US
; CURRENT APPLICATION NUMBER: US/11/187,687
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: 60/590,035
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: 60/659,709
; PRIOR FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 28
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-24

Query Match      58.3%; Score 21; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.3e-15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30
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Db 18 EESQOQEKNEQELLELDKWA 38

RESULT 8
US-10-841-956A-4
; Sequence 4, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-10-841-956A-4

Query Match      58.3%; Score 21; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30
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Db 241 EESQOQEKNEQELLELDKWA 261

RESULT 9
US-10-841-956A-8
; Sequence 8, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
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; SEQ ID NO 7
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-841-956A-7

Query Match          58.3%; Score 21; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0;

QY      10 EESNQOEKNEQELLELDKWA 30
      |||||||
DB      10 EESNQOEKNEQELLELDKWA 30

RESULT 12
US-10-841-956A-6
; Sequence 6, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-841-956A-6

Query Match          58.3%; Score 21; DB 6; Length 282;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0;

QY      10 EESNQOEKNEQELLELDKWA 30
      |||||||
DB      256 EESNQOEKNEQELLELDKWA 276

RESULT 13
US-10-841-956A-9
; Sequence 9, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59

```

; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-841-956A-9

Query Match 58.3%; Score 21; DB 6; Length 293;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWA 30
|||||
DB 267 EESQNOEKNEQELLELDKWA 287

RESULT 14

US-11-053-100-27
; Sequence 27, Application US/11053100
; Publication No. US2005025554A1
; GENERAL INFORMATION:
; APPLICANT: CHILKOTI, Ashutosh
; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
; FILE REFERENCE: 4176-101 CIP
; CURRENT APPLICATION NUMBER: US/11/053,100
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 09/812,382
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,659
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(354)
; OTHER INFORMATION: pET15b-ELP4-60-EK-T20 peptide
US-11-053-100-27

Query Match 58.3%; Score 21; DB 7; Length 354;
Best Local Similarity 100.0%; Pred. No. 2.4e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWA 30
|||||
DB 328 EESQNOEKNEQELLELDKWA 348

RESULT 15

US-11-053-100-36
; Sequence 36, Application US/11053100
; Publication No. US2005025554A1
; GENERAL INFORMATION:
; APPLICANT: CHILKOTI, Ashutosh
; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
; FILE REFERENCE: 4176-101 CIP
; CURRENT APPLICATION NUMBER: US/11/053,100
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 09/812,382
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,659
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36

; LENGTH: 356
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(356)
; OTHER INFORMATION: pET17b-ELP4-60-TEV(Q/Y)-T20 peptide
US-11-053-100-36

Query Match 58.3%; Score 21; DB 7; Length 356;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWA 30
|||||
DB 330 EESQNOEKNEQELLELDKWA 350

Search completed: March 6, 2006, 16:33:25
Job time : 10.3333 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:31:26 ; Search time 114.667 Seconds
(without alignment)
137.945 Million cell updates/sec

Title: US-09-809-060A-4
Perfect score: 192
Sequence: 1 YTSLLVSLLEKSIQKEKNEQELLELDKWSLWNP 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	100.0	36	3 AAY89840	Aay89840 Core poly
2	192	100.0	36	3 AAY89841	Aay89841 Core poly
3	192	100.0	36	4 AAB78242	Aab78242 Core poly
4	192	100.0	36	4 AAB78241	Aab78241 Core poly
5	192	100.0	36	4 AAU70182	Aau70182 HIV viral
6	192	100.0	36	4 ABB01248	Abb01248 Viral DP1
7	192	100.0	36	4 ABB01249	Abb01249 Viral DP1
8	192	100.0	36	4 ABB02833	Abb02833 Viral cor
9	192	100.0	36	4 AAU13794	Aau13794 DP178-lik
10	192	100.0	36	4 AAU13795	Aau13795 DP178-lik
11	192	100.0	36	5 AAO18774	Aao18774 HIV gp41
12	192	100.0	36	5 AAO18826	Aao18826 HIV gp41
13	192	100.0	36	5 ADE02854	Ade02854 Hybrid po
14	192	100.0	36	5 ADE02853	Ade02853 Hybrid po
15	192	100.0	36	8 ADN06925	Adn06925 Peptide #
16	192	100.0	36	8 ADS87260	Ads87260 HIV-1 gp4
17	192	100.0	36	9 ADY71547	Ady71547 HIV-1 tra
18	192	100.0	36	9 ABB02834	Abb02834 Viral cor
19	189	98.4	36	4 AAR98401	Aar98401 Peptide c
20	187	97.4	36	2 AAW17014	Aaw17014 DP-178-lik
21	187	97.4	36	2 AAB54788	Aab54788 HIV antiv
22	187	97.4	36	4 AAB92247	Aab92247 Virus rel
23	187	97.4	36	4 AAG67042	Aag67042 HIV-1 gp4
24	187	97.4	36	4 AAG67042	Aag67042 HIV-1 gp4

25	187	97.4	36	4 AAU14014	Aau14014 DP178 hom
26	187	97.4	36	6 ABO10166	Abol10166 HIV1-NV g
27	181	94.3	36	3 AAY89911	Aay89911 Core poly
28	181	94.3	36	4 AAB78312	Aab78312 Core poly
29	181	94.3	36	4 ABB01319	Abb01319 Viral DP1
30	181	94.3	36	4 AAU13865	Aau13865 DP178-lik
31	181	94.3	36	5 ADE02837	Ade02837 Hybrid po
32	180	93.8	48	8 ADU80515	Adu80515 Transmemb
33	180	93.8	48	9 ADZ40273	Adz40273 HIV-1 gp4
34	179	93.2	36	4 AAB77633	Aab77633 Core poly
35	179	93.2	36	4 ABB02115	Abb02115 Viral cor
36	179	93.2	36	4 ABB00638	Abb00638 Viral DP1
37	179	93.2	36	4 AAU13186	Aau13186 DP178-lik
38	179	93.2	36	5 ADE02135	Ade02135 Hybrid po
39	179	93.2	36	8 ADG13553	Adg13553 HIV gp41
40	179	93.2	48	8 ADU80509	Adu80509 Transmemb
41	179	93.2	48	9 ADZ40267	Adz40267 HIV-1 gp4
42	178	92.7	36	4 AAB77634	Aab77634 Core poly
43	178	92.7	36	4 ABB00639	Abb00639 Viral DP1
44	178	92.7	36	4 ABB02116	Abb02116 Viral cor
45	178	92.7	36	4 AAU13187	Aau13187 DP178-lik

ALIGNMENTS

RESULT 1

AAy89840
ID AAY89840 standard; peptide; 36 AA.
XX
AC AAY89840;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 1409.
XX
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KW anti-fusogenic; differentiation factor; interleukin; interferon;
KW colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
FN WO9959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
XX WPI; 2000-136792/12.
XX
A new hybrid polypeptide with enhanced pharmacokinetic properties
comprises enhancer sequence.
XX
PS Disclosure; Page 45; 124pp; English.
XX
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
sequence linked to core polypeptides. The enhancer polypeptides are
derived from various retroviral envelope (gp41) protein sequences,
especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
pharmacokinetic properties such as increasing the half-life of any core
polypeptide that they are linked to. The core polypeptides are any
polypeptide that may be introduced into a living system and that can
function as a pharmacologically useful peptide for the treatment or
prevention of a disease. The core polypeptides are bioactive peptides
selected from a growth factor, cytokine, differentiation factor,
interleukin, interferon, colony stimulating factor, hormone or angiogenic

XX DE Viral DP178/107-like region peptide T1409.
XX XX
XX KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
XX infection.
XX OS
XX Viruses.
XX XX
XX FT Key Location/Qualifiers
FT Modified-site 1
FT FT /note= "N-terminal is substituted by Ac"
FT Modified-site 36
FT FT /note= "C-terminal amide"
XX
XX WO200164013-A2.
XX
XX 07-SEP-2001.
XX
XX 07-FEB-2001; 2001WO-US003988.
XX
XX 29-FEB-2000; 2000US-00515965.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX PA Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX WPI; 2001-514829/56.
XX
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
XX fusion, useful for treating HIV and Respiratory Syncytial Virus
XX infection.
XX
XX Disclosure; Page 58; 587pp; English.
XX
XX The invention relates to isolated analogues of the heptad repeat region
XX peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
XX 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
XX respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
XX regions of proteins interact non-covalently with each other and/or with
XX peptides derived from them. This interaction is required for normal
XX infectivity of viruses such as RSV and HIV. The heptad repeat region
XX peptide analogues may be used to inhibit respiratory syncytial virus
XX (RSV) infection in a cell. They may also be used to inhibit HIV
XX infection. The present sequence is a peptide provided in the
XX specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
XX 11-SEP-2003 to standardise OS field)
XX SQ Sequence 36 AA;
XX
XX Query Match 100.0%; Score 192; DB 4; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-16;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YTSLIYSLLSKSQIQQEKNEQLLELDKWASLWNWF 36
XX |||||
XX DB 1 YTSLIYSLLSKSQIQQEKNEQLLELDKWASLWNWF 36
XX
XX RESULT 7
XX ABB01249
XX ID ABB01249 standard; peptide; 36 AA.
XX
XX AC ABB01249;
XX
XX 11-SEP-2003 (revised)
XX 06-AUG-2003 (revised)
XX 03-JAN-2002 (first entry)
XX
XX Viral DP178/107-like region peptide T1410.
XX
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
XX virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
XX infection.

KW infection.
XX Viruses.
XX WO200164013-A2.
XX
XX 07-SEP-2001.
XX
XX 07-FEB-2001; 2001WO-US003988.
XX
XX 29-FEB-2000; 2000US-00515965.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX WPI; 2001-514829/56.
XX
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
XX fusion, useful for treating HIV and Respiratory Syncytial Virus
XX infection.
XX
XX Disclosure; Page 58; 587pp; English.
XX
XX The invention relates to isolated analogues of the heptad repeat region
XX peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
XX 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
XX respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
XX regions of proteins interact non-covalently with each other and/or with
XX peptides derived from them. This interaction is required for normal
XX infectivity of viruses such as RSV and HIV. The heptad repeat region
XX peptide analogues may be used to inhibit respiratory syncytial virus
XX (RSV) infection in a cell. They may also be used to inhibit HIV
XX infection. The present sequence is a peptide provided in the
XX specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
XX 11-SEP-2003 to standardise OS field)
XX SQ Sequence 36 AA;
XX
XX Query Match 100.0%; Score 192; DB 4; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-16;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YTSLIYSLLSKSQIQQEKNEQLLELDKWASLWNWF 36
XX |||||
XX DB 1 YTSLIYSLLSKSQIQQEKNEQLLELDKWASLWNWF 36
XX
XX RESULT 8
XX ABB02833
XX ID ABB02833 standard; peptide; 36 AA.
XX
XX AC ABB02833;
XX
XX 11-SEP-2003 (revised)
XX 06-AUG-2003 (revised)
XX 03-JAN-2002 (first entry)
XX
XX Viral core polypeptide, SEQ ID NO: 1360.
XX
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
XX virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
XX infection.
XX Viruses.
XX OS
XX WO200164013-A2.
XX
XX 07-SEP-2001.
XX
XX 07-FEB-2001; 2001WO-US003988.
XX
XX 29-FEB-2000; 2000US-00515965.
XX

XX PA (TRIM-) TRIMERIS INC.
XX PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX PS WPI; 2001-514829/56.
XX PT Heptad repeat region peptide analogs useful for inhibiting virus/cells
XX FT fusion, useful for treating HIV and Respiratory Syncytial Virus
XX PS infection.
XX PS Disclosure; Page 525; 587pp; English.
XX CC The invention relates to isolated analogues of the heptad repeat region
XX CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
XX CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
XX CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
XX CC regions of proteins interact non-covalently with each other and/or with
XX CC peptides derived from them. This interaction is required for normal
XX CC infectivity of viruses such as RSV and HIV. The heptad repeat region
XX CC peptide analogues may be used to inhibit respiratory syncytial virus
XX CC (RSV) infection in a cell. They may also be used to inhibit HIV
XX CC infection. The present sequence is a peptide provided in the
XX CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
XX CC 11-SEP-2003 to standardise OS field)
XX SQ Sequence 36 AA;
Query Match 100.0%; Score 192; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTSLIYSLEKSIQIQEKNEQELLELDKWSLWNWF 36
Db 1 YTSLIYSLEKSIQIQEKNEQELLELDKWSLWNWF 36
RESULT 9
AAU13794
ID AAU13794 standard; peptide; 36 AA.
XX AC AAU13794;
XX DT 21-NOV-2001 (first entry)
XX DE DP178-like/DP107-like peptide T-1409.
XX KW Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
XX KW antifusogenic; antiviral; HIV transmission; mutant; mutein.
XX OS Human immunodeficiency virus 1; isolate LAI.
XX OS Synthetic.
FH Key Location/Qualifiers
FT Modified-site 1
FT FT /note= "N-terminal is substituted by Ac"
FT FT Modified-site 36
FT FT /note= "C-terminal amide"
XX XX
XX PN WO200151673-A2.
XX XX
XX PD 19-JUL-2001.
XX XX
XX PF 05-JUL-2000; 2000WO-US035727.
XX PR 09-JUL-1999; 99US-00350841.
XX XX (TRIM-) TRIMERIS INC.
XX PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX CC

PT Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
XX DP107/DP178 complex.
XX PS Disclosure; Page 77; 259pp; English.
XX CC The present invention relates to peptides which exhibit anti-retroviral
XX CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
XX CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
XX CC amino acids 639-673 of the transmembrane protein gp41 from human
XX CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
XX CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
XX CC also relates to a method of identifying compounds that inhibit the
XX CC formation of or disrupts a DP107/DP178 complex. The method comprises
XX CC detecting the formation of a DP107/DP178 complex, both in the presence or
XX CC absence of a test compound, in a reaction mixture containing DP107 and
XX CC DP178 peptides. The method is useful for identifying compounds, including
XX CC small molecule compounds, which may themselves exhibit antifusogenic,
XX CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
XX CC peptides are useful to inhibit human and non-human retroviral,
XX CC particularly HIV, transmission to uninfected cells. The present sequence
XX CC represents one of the DP178-like/DP107-like peptides of the invention
XX SQ Sequence 36 AA;
Query Match 100.0%; Score 192; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTSLIYSLEKSIQIQEKNEQELLELDKWSLWNWF 36
Db 1 YTSLIYSLEKSIQIQEKNEQELLELDKWSLWNWF 36
RESULT 10
AAU13795
ID AAU13795 standard; peptide; 36 AA.
XX AC AAU13795;
XX DT 21-NOV-2001 (first entry)
XX DE DP178-like/DP107-like peptide T-1410.
XX KW Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
XX KW antifusogenic; antiviral; HIV transmission; mutant; mutein.
XX OS Human immunodeficiency virus 1; isolate LAI.
XX OS Synthetic.
XX PN WO200151673-A2.
XX XX
XX PD 19-JUL-2001.
XX PF 05-JUL-2000; 2000WO-US035727.
XX PR 09-JUL-1999; 99US-00350841.
XX XX (TRIM-) TRIMERIS INC.
XX PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX CC Identifying a compound that inhibits the formation of or disrupts a
XX CC DP107/DP178 complex, especially compounds with antifusogenic, antiviral
XX CC or intracellular modulatory activity, by detecting the formation of a
XX CC DP107/DP178 complex.
XX PS Disclosure; Page 77; 259pp; English.
XX CC The present invention relates to peptides which exhibit anti-retroviral

CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupt a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents one of the DP178-like/DP107-like peptides of the invention
XX
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 192; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |
Db 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 11

AAO18774
ID AAO18774 standard; peptide; 36 AA.

XX AAO18774;

XX 29-OCT-2002 (first entry)

XX HIV gp41 protein DP-178 region derived peptide SEQ ID NO: 5.

XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
XX gp41.

XX Human immunodeficiency virus.

XX WO200256902-A2.

XX 25-JUL-2002.

XX 17-DEC-2001; 2001WO-US048802.

XX 19-DEC-2000; 2000US-0256657P.

XX (SCHE) SCHERING CORP.

XX Baroudy BM;

XX WPI; 2002-636513/68.

XX Treatment of HIV infection in an individual involves administration of a
XX combination of chemokine co-receptor five antagonist and a specified HIV
XX envelope polypeptide.

XX Disclosure; Page 32; 52pp; English.

XX The present invention relates to a method of treating an HIV infection in
XX an individual, which involves administering in combination a chemokine co
XX -receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
XX derivative. Other viral infections can also be treated using the method.
XX The present sequence is a peptide derived from HIV and useful in the
XX method of the invention

XX Sequence 36 AA;

Query Match 100.0%; Score 192; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |
Db 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 12

AAO18826
ID AAO18826 standard; peptide; 36 AA.

XX AAO18826;

XX 29-OCT-2002 (first entry)

XX HIV gp41 protein DP-178 region derived peptide SEQ ID NO: 57.

XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
XX gp41.

XX Human immunodeficiency virus.

XX WO200256902-A2.

XX 25-JUL-2002.

XX 17-DEC-2001; 2001WO-US048802.

XX 19-DEC-2000; 2000US-0256657P.

XX (SCHE) SCHERING CORP.

XX Baroudy BM;

XX WPI; 2002-636513/68.

XX Treatment of HIV infection in an individual involves administration of a
XX combination of chemokine co-receptor five antagonist and a specified HIV
XX envelope polypeptide.

XX Disclosure; Page 34; 52pp; English.

XX The present invention relates to a method of treating an HIV infection in
XX an individual, which involves administering in combination a chemokine co
XX -receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
XX derivative. Other viral infections can also be treated using the method.
XX The present sequence is a peptide derived from HIV and useful in the
XX method of the invention

XX Sequence 36 AA;

Query Match 100.0%; Score 192; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |
Db 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 13

ADE02854
ID ADE02854 standard; peptide; 36 AA.

XX ADE02854;

XX 29-JAN-2004 (first entry)

XX Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID NO 1361.

XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;
XX pharmacokinetic; fusogenic; insulin; diabetes.

	/note= "C-terminal amide"
FT	US6348568-B1.
XX	19-FEB-2002.
XX	20-MAY-1999; 99US-00315304.
PF	20-MAY-1998; 98US-00082279.
XX	(TRIM-) TRIMERIS INC.
PA	Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
PI	WPI; 2002-424396/45.
XX	New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope protein sequences linked to core polypeptide e.g. therapeutic protein.
PT	Disclosure; SEQ ID NO 1360; 70pp; English.
PS	The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WQWEKQI or WASLMEWF. The invention also includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel hybrid polypeptide has virucide and antidiabetic activity. The enhancer peptide sequence enhances pharmacokinetic properties of any core polypeptide, for example, a polypeptide useful for the treatment or prevention of a disease, or an imaging agent useful for imaging structures in vivo. The core polypeptides and hybrid polypeptides are useful for modulating fusogenic events and inhibit antifusogenic or antiviral activity. The novel hybrid polypeptide is useful for decreasing viral infection and modulating intracellular processes involving coiled-coil peptide interactions. The novel hybrid polypeptide comprises insulin or its fragment, so the core polypeptide is useful for ameliorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also useful as a part of prognosis for preventing disorders including fusion events and viral infection that involves cell-cell and/or virus-cell fusion, and for diagnosis and in vivo imaging methods. This sequence represents an enhancer peptide of the invention.
CC	SX Sequence 36 AA;
Query Match	100.0%; Score 192; DB 5; Length 36;
Best Local Similarity	100.0%; Pred. No. 2.1e-16;
Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 YTSLLYSLEKSQIQEQEKNEQLLEDKWASLNWNF 36
Dd	1 YTSLLYSLEKSQIQEQEKNEQLLEDKWASLNWNF 36
RESULT 15	
ADN06925	
ID	ADN06925 standard; peptide; 36 AA.
AC	ADN06925;
DT	17-JUN-2004 (first entry)
DE	Peptide #36 used in the pharmaceutical composition of the invention.
KW	Pharmaceutical; human immunodeficiency virus; HIV; gp41; glycoprotein41;
XV	HIV infection; antiviral; therapy.
OS	Unidentified.
FN	US2004063637-A1.
PD	01-APR-2004.
XX	

Unidentified.	
XX	US6348568-B1.
PN	19-FEB-2002.
PD	20-MAY-1999; 99US-00315304.
XX	20-MAY-1998; 98US-00082279.
PP	(TRIM-) TRIMERIS INC.
XX	Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
PI	WPI; 2002-424396/45.
DR	New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope protein sequences linked to core polypeptide e.g. therapeutic protein.
XX	Disclosure; SEQ ID NO 1361; 70pp; English.
PS	The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WQWEKQI or WASLMEWF. The invention also includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel hybrid polypeptide has virucide and antidiabetic activity. The enhancer peptide sequence enhances pharmacokinetic properties of any core polypeptide, for example, a polypeptide useful for the treatment or prevention of a disease, or an imaging agent useful for imaging structures in vivo. The core polypeptides and hybrid polypeptides are useful for modulating fusogenic events and inhibit antifusogenic or antiviral activity. The novel hybrid polypeptide is useful for decreasing viral infection and modulating intracellular processes involving coiled-coil peptide interactions. The novel hybrid polypeptide comprises insulin or its fragment, so the core polypeptide is useful for ameliorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also useful as a part of prognosis for preventing disorders including fusion events and viral infection that involves cell-cell and/or virus-cell fusion, and for diagnosis and in vivo imaging methods. This sequence represents an enhancer peptide of the invention.
CC	SX Sequence 36 AA;
Query Match	100.0%; Score 192; DB 5; Length 36;
Best Local Similarity	100.0%; Pred. No. 2.1e-16;
Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 YTSLLYSLEKSQIQEQEKNEQLLEDKWASLNWNF 36
Dd	1 YTSLLYSLEKSQIQEQEKNEQLLEDKWASLNWNF 36
RESULT 14	
ADE02853	
ID	ADE02853 standard; peptide; 36 AA.
AC	ADE02853;
DT	29-JAN-2004 (first entry)
DE	Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID NO 1360.
KW	hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;
XV	pharmacokinetic; fusogenic; insulin; diabetes.
OS	Unidentified.
FN	Key Location/Qualifiers
PH	Modified-site 1
FT	/note= "Residue is modified by acetyl group"
FT	Modified-site 36
XX	

PF 16-SEP-2003; 2003US-00663589.
XX
PR 27-SEP-2002; 2002US-0414441P.
XX
PA (HEIL/) HEILMAN D.
PA (DIJJ/) DI J.
PA (BRAY/) BRAY B.
XX
PI Heilman D, Di J, Bray B;
XX
XX WPI; 2004-339372/31.
DR
XX
XX Pharmaceutical composition used to treat Human Immunodeficiency Virus
PT comprises solution comprising synthetic peptide (Human Immunodeficiency
PT Virus fusion inhibitor) in mixture with polyol.
XX
PS Disclosure; SEQ ID NO 40; 36pp; English.
XX
CC The present invention relates to a pharmaceutical composition comprised
CC of polymer admixed with synthetic peptides derived from human
CC immunodeficiency virus (HIV) gp41. The invention is useful in treating
CC HIV infection (preferably HIV-1) and act as an antiviral agent. The
CC present sequence is a peptide used in the pharmaceutical composition of
CC the invention
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 192; DB 8; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIYSLLEKSIQQEKNEQELLELDKWSLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |
DB 1 YTSLIYSLLEKSIQQEKNEQELLELDKWSLWNWF 36

Search completed: March 6, 2006, 15:37:21
Job time : 115.667 secs

GenCore version 5.1.7
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OM protein - protein_search, using sw model

Run on: March 6, 2006, 15:37:45 ; Search time 18.3333 Seconds
(without alignments)
188.935 Million cell updates/sec

Title: US-09-809-060A-4
Perfect score: 192
Sequence: 1 YTSLIYSLLEKSIQIQEKNEQELLELDKXWASLWNP 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	20.8	36	2 A34594	myosin regulatory
2	39	20.3	30	2 H70152	hypothetical prote
3	38	19.8	31	2 I50390	myosin light chain
4	37	19.3	45	2 T52125	R2R3-MYB transcrip
5	36	18.8	24	2 S01808	hemoglobin AII - t
6	36	18.8	30	2 I77411	renin-2 - mouse (f
7	36	18.8	38	2 C92373	hypothetical prote
8	36	18.8	45	2 S01814	hemoglobin BII - t
9	35	18.2	33	2 A82186	hypothetical prote
10	35	18.2	36	2 DB3682	hypothetical prote
11	35	18.2	42	2 T07291	hypothetical prote
12	35	18.2	47	2 C81237	hypothetical prote
13	35	18.2	49	2 T06923	high light-inducib
14	35	18.2	50	2 E90557	hypothetical prote
15	35	18.2	50	2 F86472	5.7K hypothetical
16	34.5	18.0	48	2 S35693	cystic fibrosis tr
17	34	17.7	40	2 S77777	hypothetical prote
18	34	17.7	41	2 T07274	hypothetical prote
19	34	17.7	41	2 T48342	hypothetical prote
20	34	17.7	45	2 S28565	hypothetical prote
21	34	17.7	47	2 G84083	hypothetical prote
22	34	17.7	50	2 P00026	photosystem I 9K p
23	33.5	17.4	43	2 B83894	hypothetical prote
24	33.5	17.4	47	2 S31005	gene 60 protein -
25	33	17.2	33	2 S23321	hypothetical prote
26	33	17.2	43	2 S21282	thymosin beta-11 -
27	33	17.2	43	2 S21694	thymosin beta-12 -
28	33	17.2	48	2 DB3774	hypothetical prote
29	33	17.2	50	2 T06541	probable NADPH-fer

30 32.5 16.9 46 2 D90534 ribosomal protein
31 32.5 16.9 49 2 A37405 androgen-binding p
32 32 16.7 43 1 TNBOB4 thymosin beta-4 -
33 32 16.7 43 2 T07503 hypothetical prote
34 32 16.7 43 2 H83653 hypothetical prote
35 32 16.7 44 1 A38682 thymosin beta-4 (v
36 32 16.7 44 1 TNRTB4 thymosin beta-4 -
37 32 16.7 49 2 E97287 L33 protein (impor
38 32 16.7 49 2 F70221 hypothetical prote
39 32 16.7 50 1 A37217 thymosin beta-4 -
40 32 16.7 50 2 A90573 50S ribosomal prot
41 31 16.1 25 2 S68897 phospholipase A2 (
42 31 16.1 28 1 LPSEW trp operon leader
43 31 16.1 29 2 E33208 calreticulin, uter
44 31 16.1 31 2 H82533 hypothetical prote
45 31 16.1 32 2 S20771 Ig heavy chain V r

ALIGNMENTS

RESULT 1

A34594
myosin regulatory light chain - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 29-Jun-1990 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C/Accession: A34594; A31967
R/Ikebe, M.; Reardon, S.
Biochemistry 29, 2713-2720, 1990
A/Title: Phosphorylation of bovine platelet myosin by protein kinase C.
A/Reference number: A34594; MUID:90268021; PMID:2346743
A/Accession: A34594
A/Molecule type: protein
A/Residues: 1-33, 'X', 35-36 <IKE>
A/Cross-references: UNIPROT:Q7M2V5; UNIPARC:UPI00001776D9
A/Experimental source: platelet
R/Colburn, J.C.; Michnoff, C.H.; Hsu, L.C.; Slaughter, C.A.; Kamm, K.E.; Stull, J.T.
J. Biol. Chem. 263, 19166-19173, 1988
A/Title: Sites phosphorylated in myosin light chain in contracting smooth muscle.
A/Reference number: A31967; MUID:89066722; PMID:3198618
A/Accession: A31967
A/Molecule type: protein
A/Residues: 17-34 <COL>
A/Cross-references: UNIPARC:UPI00001776DA
A/Experimental source: smooth muscle
C/Suprafamily: calmodulin; calmodulin repeat homology
C/Keywords: blocked amino end; EF hand; phosphoprotein
F/1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental
F/1/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experimental
F/2/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experimental
F/9/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status experimental
F/18/Binding site: phosphate (Thr) (covalent) (by myosin-light-chain kinase) (partial) #
F/19/Binding site: phosphate (Ser) (covalent) (by myosin-light-chain kinase) #status exp

Query Match 20.8%; Score 40; DB 2; Length 36;
Best Local Similarity 41.2%; Pred. No. 1.8e+02;
Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TSLIYSLLEKSIQIQEK 18
|| :||:|||||:
Db 18 TSNVFAMFDQSIQEFK 34

RESULT 2

H70152
hypothetical protein BB0425 - Lyme disease spirochete
C/Species: Borrelia burgdorferi (Lyme disease spirochete)
C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C/Accession: H70152
R/Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.
A;Reference number: A70100; PMID:98065943; PMID:9403685
A;Accession: H70152
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-30 <KLE>
A;Cross-references: UNIPROT:O51386; UNIPARC:UPI0000057491; GB:AE001147; GB:AE001147
A;Experimental source: strain B31

Query Match 20.3%; Score 39; DB 2; Length 30;
Best Local Similarity 46.7%;
Matches 7; Conservative 5; Mismatches 3; Indels
Pred. No. 2e+02;

Qy 10 EKSIOQEKNQELL 24
| | : : | : | |
Db 8 ELSKVKSQKNQONLL 22

RESULT 3

myosin light chain - chicken (fragment)

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: I50390; I50392

R/Winter, B.; Klaphor, H.; Wiesbauer, K.; Delius, H.; Arnold, H.H.

J. Biol. Chem. 260, 4478-4483, 1985

A>Title: Isolation and characterization of the chicken cardiac myosin light chain (L-2A)

A/Reference number: I50390; MUID:85157617; PMID:12984206

A/Accession: I50390

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-31 <WIN>

A/Cross-references: UNIPROT:Q91828; UNIPARC:UPI00000FD6CF; GB:M10990; NID:g212385; PIDN:R/Zarraga, A.

J. Biol. Chem. 261, 13852-13860, 1986

A>Title: Characterization of 5'-flanking region of myosin light chain 2A gene: Structural

A/Reference number: I50392; MUID:87008629; PMID:13020054

A/Accession: I50392

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-31 <ZAR>

A/Cross-references: UNIPARC:UPI00000FD6CF; GB:J02587; NID:g212390; PIDN:AAA48977.1; PID: C/Genetics:

A/Introns: 1/3

C/Superfamily: calmodulin; calmodulin repeat homology

C/Keywords: EF hand

Query Match	19.8%	Score 38;	DB 2;	Length 31;
Best Local Similarity	43.8%	Pred. No. 2.7e+02;		
Matches	7;	Conservative	6;	Mismatches 3;
				Indels 0;
				Gaps 0;

Qy 3 SLIYSLLEKSQIQEK 18
 | : : : | : : : |
Db 15 SNVFSMFEOAQIOEFK 30

RESULT 4
T52125
R2R3-MYB transcription factor [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52125; T52126
R;Romero, I.; Fuentes, A.; Benito, M.J.; Malpica, J.; Leyva, A.; Paz-Ares, J.
submitted to the EMBL Data Library, May 1997
A;Description: One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.
A;Reference number: Z25968

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-45 -cRo2>
A;Cross-references: UNIPARC:UPI000016DC6F; EMBL:Z95788; PIDN:CAB09220.1
C;Genetics:
A;Gene: MYB56; MYB65

Query Match	19.3%	Score 37;	DB 2;	Length 45;
Best Local Similarity	34.5%	Pred. No. 5.5e+02;		
Matches 10;	Conservative	7;	Mismatches 6;	Indels 6;
				Gaps 2;

QY	9 LEKSIQQEKNEQELLEL-----DKWASL 32 : : :
Db	11 LKKGAFSQEE-EQLIVEMHAKMGNKWAQM 38 : : :

RESULT 5
S01808
hemoglobin AII - tube worm (Lamellibrachia sp.) (fragment)
C/Species: Lamellibrachia sp.
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: S01808
R/Suzuki, T.; Takagi, T.; Ohta, S.
Biochem. J. 255, 541-545, 1988
A/Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin
A/Reference number: S01807; MUID:89076216; PMID:3202832
A/Accession: S01808
A/Molecule type: protein
A/Residues: 1-24 <SUZ>
A/Cross-references: UNIPROT:Q9TWS6; UNIPARC:UPI000017711B
C/Keywords: oxvaen carrier

Query Match 18.8%; Score 36; DB 2; Length 24;
Best Local Similarity 26.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 8; Mismatches 2; Indels 4; Gaps 1;

```

Qy      16 QEKNEQELLELDKWASLWN 34
Db      8 EDRREMQLM----WANVWS 22

```

RESULT 6
I77411
renin-2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C:Accession: I77411
R:field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.
Mol. Cell. Biol. 4, 2321-2331, 1984
A:title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparison
A:reference number: I57576; MUID:85085936; PMID:6392850
A:Accession: I77411
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-30 <RES>
A:Cross-references: UNIPROT:P00796; UNIPARC:UPI000016C94B; GB:K02801; NID:P
C:Superfamily: Pepsin

Query Match	18.8%;	Score 36;	DB 2;	Length 30;
Best Local Similarity	71.4%;	Pred. No. 4.6e+02;		
Matches 5;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;			

Qy	29	WASLWNW	35
Db	9	WALLWLW	15

RESULT 7
C82373 hypothetical protein VC0017 [imported] - Vibrio cholerae (strain Ni6961 serogroup O1)
C;Species: Vibrio cholerae
C;date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C82373

Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: C01237
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-47 <TET>
A:Cross-references: UNIPROT:Q9K1L4; UNIPARC:UPI000000C43EE; GB:AE002098; NID
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0099

Query Match 18.2%; Score 35; DB 2; Length 47;
Best Local Similarity 37.5%; Pred. No. 1.le+03;
Matches 9; Conservative 3; Mismatches 8; Indels 4; Gaps 1;

Qy 10 EKSQIQ---EKNEQEELLELDKW 29
:|||||:|:|:
Db 20 KKQIQQKKETKSPKHKASRDDW 43

RESULT 13
T06923
high light-inducible protein homolog - Cyanophora paradoxa cyanelle
C:Species: cyanelle Cyanophora paradoxa
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06923
R:Stirewalt, V.L.; Michaloweki, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.
submitted to the EMBL Data Library, July 1995
A:Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
A:Reference number: Z15840
A:Accession: T06923

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-49 <STI>
A:Cross-references: UNIPROT:P48367; UNIPARC:UPI000013A441; EMBL:U30821; NID:gi1016083; PI
A:Experimental source: strain Pringsheim LB555
C:Genetics:
A:Gene: ycf17
A:Genome: cyanelle
C:Superfamily: high light-inducible protein ssl2542
C:Keywords: cyanelle

Query Match 18.2%; Score 35; DB 2; Length 49;
Best Local Similarity 27.3%; Pred. No. 1.le+03;
Matches 6; Conservative 4; Mismatches 0; Indels 12; Gaps 1;

Qy 14 IQEKNQEELLELDKWASLWNW 35
:|||||:|:|:
Db 1 MQEERN-----IWNW 10

RESULT 14
E90557
hypothetical protein MYPV 3650 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: E90557
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: E90557
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <KUR>
A:Cross-references: UNIPROT:Q98QJ6; UNIPARC:UPI000000C8071; GB:AL445566; PTD:gi14089779; F
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPV_3650
A:Genetic code: SGC3

Query Match 18.2%; Score 35; DB 2; Length 50;
Best Local Similarity 33.3%; Pred. No. 1.le+03;
Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 5 IYSLLEKSIQOEKNEQEELLELDK 28
:|||||:|:|:
Db 6 LYENIKKEIKYKNSIVLNEFKK 29

RESULT 15
F86472
5.7K hypothetical protein T3269.50 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86472
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86472

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <STO>
A:Cross-references: UNIPROT:Q9C6E9; UNIPARC:UPI000000A80F1; GB:AE005172; NID:gi11386311; P:
C:Genetics:
A:Map position: 1

Query Match 18.2%; Score 35; DB 2; Length 50;
Best Local Similarity 38.1%; Pred. No. 1.le+03;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 7 SLLEKSIQOEKNEQEELLELD 27
:|||||:|:|:
Db 17 SYQFESETESESEDEETESD 37

Search completed: March 6, 2006, 15:44:17
Job time : 19.3333 secs


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OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=94211861; PubMed=7512731;
RX Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06726; AAA19139.1; -; mRNA.
DR HSSP; P31872; 1LBO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 49
FT NON TER 49 49
SQ SEQUENCE 49 AA; 6167 MW; 0277C4815B8D26FE CRC64;

Query Match 94.3%; Score 181; DB 2; Length 49;
Best Local Similarity 91.7%; Pred. No. 1.1e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36
Db 14 YTGLIYTLLEESQIQQEKNEQELLELDKWASLWNWF 49

RESULT 3
O69909_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06739; AAA19152.1; -; mRNA.
DR HSSP; P31872; 1LBO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 49
FT NON TER 49 49
SQ SEQUENCE 49 AA; 6196 MW; E9B618025B832D1E CRC64;

Query Match 92.7%; Score 178; DB 2; Length 49;
Best Local Similarity 91.7%; Pred. No. 2.5e-14;
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36
Db 14 YTGLIYTLLEESQIQQEKNEQELLELDKWASLWNWF 49

RESULT 4

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O69910_9HIV1 PRELIMINARY; PRT; 42 AA.
AC Q69910;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06740; AAA19153.1; -; mRNA.
DR HSSP; P31872; 1LBO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 42
FT NON TER 42 42
SQ SEQUENCE 42 AA; 5248 MW; 613E1B2DBB31A722 CRC64;

Query Match 91.7%; Score 176; DB 2; Length 42;
Best Local Similarity 88.9%; Pred. No. 3.7e-14;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36
Db 7 YTSLIYTLLEESQIQQEKNEQELLELDKWASLWNWF 42

RESULT 5
O69906_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69906;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06736; AAA19149.1; -; mRNA.
DR HSSP; P31872; 1LBO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 49
FT NON TER 49 49
SQ SEQUENCE 49 AA; 6214 MW; 29C4E5A8CBD63DD8 CRC64;

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Query Match          90.6%; Score 174; DB 2; Length 49;
Best Local Similarity 86.1%; Pred.No.7.8e-14;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 YTSLIYLLKKSQIQEQKNEQELLELDKWASLWNWF 36
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      14 YTSLIYTLIESQIQEQKNEKELLELDKWASLWNWF 49

RESULT 6
Q69907_9HIV1
ID      Q69907_9HIV1 PRELIMINARY;          PRT;      49 AA.
AC      Q69907;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Gp41 (Fragment).
GN      Name=env;
GS      Human immunodeficiency virus 1.
OS      Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC      Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
RN      [1].
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=94211861; PubMed=7512731;
RA      Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA      Keller P.M., Shaw A.R., Emini E.A.;
RT      "Neutralization of divergent human immunodeficiency virus type 1
RT      variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT      monoclonal antibody.";
RL      Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR      ENBL; U06737; AAA19150.1; -; mRNA.
DR      HSPG; Q87973; 2SIV.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0019031; C:viral envelope; IEA.
DR      GO; GO:0005198; F:structural molecule activity; IEA.
DR      InterPro; IPR000328; Env_Gp41.
DR      Pfam; PF00517; Gp41; 1.
FT      NON_TER 1
FT      NON_TER 49
SQ      SEQUENCE 49 AA; 6241 MW; 29C4ESA8CBC7CDD8 CRC64;

Query Match          89.1%; Score 171; DB 2; Length 49;
Best Local Similarity 83.3%; Pred.No.1.8e-13;
Matches 30; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 YTSLIYLLKKSQIQEQKNEQELLELDKWASLWNWF 36
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      14 YTSLIYTLIESQIQEQKNEKELLELDKWASLWNWF 49

RESULT 7
Q69893_9HIV1
ID      Q69893_9HIV1 PRELIMINARY;          PRT;      34 AA.
AC      Q69893;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Gp41 (Fragment).
GN      Name=env;
GS      Human immunodeficiency virus 1.
OS      Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC      Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
RN      [1].
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=94211861; PubMed=7512731;
RA      Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA      Keller P.M., Shaw A.R., Emini E.A.;
RT      "Neutralization of divergent human immunodeficiency virus type 1
RT      variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT      monoclonal antibody.";

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OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06724; AAA19137.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 34
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4182 MW; A37CAA60A164B9F0 CRC64;

Query Match 87.5%; Score 168; DB 2; Length 34;
Best Local Similarity 90.9%; Pred. No. 2.9e-13;
Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LIYSLLKSKQIQOEKNEQELLELDKWSLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |
Db 2 LIYTLLESQVQOEKNEQELLELDKWSLWNWF 34

RESULT 10
Q69905_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69905;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06735; AAA19148.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 34
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4196 MW; 7B724A8EA164B99C CRC64;

Query Match 86.5%; Score 166; DB 2; Length 34;
Best Local Similarity 93.9%; Pred. No. 5e-13;
Matches 31; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 LIYSLLKSKQIQOEKNEQELLELDKWSLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |
Db 2 LIYTLLESQVQOEKNEQELLELDKWSLWNWF 34

RESULT 11
Q69903_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69903;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06733; AAA19146.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 34
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4226 MW; E609273F6164BD80 CRC64;

Query Match 85.4%; Score 164; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 8.9e-13;
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SLIYSLLKSKQIQOEKNEQELLELDKWSLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SIIYTLLESQVQOEKNEKELLELDKWSLWNWF 34

RESULT 12
Q69898_9HIV1 PRELIMINARY; PRT; 50 AA.
AC Q69898;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06728; AAA19141.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 50
FT NON_TER 50 50
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SQ SEQUENCE 50 AA; 6358 MW; EABA093A1C6C79E1 CRC64;
Query Match 84.9%; Score 163; DB 2; Length 50;
Best Local Similarity 80.6%; Pred. No. 1.8e-12;
Matches 29; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 YTSIYLSLEKSOIQEKNEQELLELDKQASLWNWF 36
|||:||||:||||:||||:||||:||||:||||:
Db 15 YTGVIYNLLESQKQEKNEQDILLDKWANLWNWF 50

RESULT 13
Q69904_9HIV1
ID Q69904_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69904;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06734; AAA19147.1; -; mRNA.
DR HSSP; P31872; 1L80.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; Gp41; 1.
FT NON TER 1
FT NON TER 34
FT NON TER 34
SQ SEQUENCE 34 AA; 4184 MW; BB1CAA65F131AD5A CRC64;
Query Match 82.3%; Score 158; DB 2; Length 34;
Best Local Similarity 84.8%; Pred. No. 4.8e-12;
Matches 28; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 4 LIYSLSLEKSOIQEKNEQELLELDKQASLWNWF 36
|||:||||:||||:||||:||||:||||:
Db 2 LIYTLIESQKQEKNEQELLELDKQASLWNWF 34

RESULT 14
Q69899_9HIV1
ID Q69899_9HIV1 PRELIMINARY; PRT; 50 AA.
AC Q69899;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human

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RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06729; AAA19142.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; Gp41; 1.
FT NON TER 1
FT NON TER 50
FT NON TER 50
SQ SEQUENCE 50 AA; 6287 MW; EABA093F0877D85B CRC64;
Query Match 81.8%; Score 157; DB 2; Length 50;
Best Local Similarity 77.8%; Pred. No. 9.8e-12;
Matches 28; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 1 YTSIYLSLEKSOIQEKNEQELLELDKQASLWNWF 36
|||:||||:||||:||||:||||:||||:
Db 15 YTGVIYNLLESQKQEKNEQDILLDKWANLWNWF 50

RESULT 15
Q69900_9HIV1
ID Q69900_9HIV1 PRELIMINARY; PRT; 50 AA.
AC Q69900;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06730; AAA19143.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; Gp41; 1.
FT NON TER 1
FT NON TER 50
FT NON TER 50
SQ SEQUENCE 50 AA; 6300 MW; EABA093F086C79E1 CRC64;
Query Match 81.8%; Score 157; DB 2; Length 50;
Best Local Similarity 77.8%; Pred. No. 9.8e-12;
Matches 28; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 1 YTSIYLSLEKSOIQEKNEQELLELDKQASLWNWF 36
|||:||||:||||:||||:||||:||||:
Db 15 YTGVIYNLLESQKQEKNEQDILLDKWANLWNWF 50

Search completed: March 6, 2006, 15:43:16
Job time : 117.667 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:43:35 ; Search time 27.6667 Seconds
(without alignments)
107.578 Million cell updates/sec

Title: US-09-809-060A-4

Perfect score: 192

Sequence: 1 YTSLLYSLLEKSIQIQEKNQELLEDKWSLWNWP 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pap:**
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pap:**
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pap:**
- 4: /cgn2_6/ptodata/1/iaa/PTCUS COMB.pap:**
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pap:**
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	100.0	36	2	US-08-484-223B-240
2	192	100.0	36	2	US-09-082-279B-1360
3	192	100.0	36	2	US-09-315-304B-1360
4	192	100.0	36	2	US-09-834-784-1360
5	192	100.0	36	2	US-09-515-965A-1360
6	192	100.0	36	2	US-09-350-641C-1360
7	192	100.0	36	2	US-09-350-841A-1360
8	189	98.4	36	2	US-09-082-279B-1361
9	189	98.4	36	2	US-09-315-304B-1361
10	189	98.4	36	2	US-09-834-784-1361
11	189	98.4	36	2	US-09-515-965A-1361
12	189	98.4	36	2	US-09-350-641C-1361
13	189	98.4	36	2	US-09-350-841A-1361
14	187	97.4	36	1	US-08-073-028-5
15	187	97.4	36	2	US-08-486-099-5
16	187	97.4	36	2	US-08-360-107A-5
17	187	97.4	36	2	US-08-484-223B-5
18	187	97.4	36	2	US-08-919-597-5
19	187	97.4	36	2	US-08-475-668A-5
20	187	97.4	36	2	US-08-485-551A-5
21	187	97.4	36	2	US-08-471-913A-5
22	187	97.4	36	2	US-08-554-616-5
23	187	97.4	36	2	US-08-485-264A-5
24	187	97.4	36	2	US-08-474-349A-5
25	187	97.4	36	2	US-08-255-208A-5
26	187	97.4	36	2	US-08-973-952-5
27	187	97.4	36	2	US-08-470-896-5

28	187	97.4	36	2	US-08-485-546A-5	Sequence 5, Appli
29	187	97.4	36	2	US-09-515-965A-1553	Sequence 1553, Ap
30	187	97.4	36	2	US-09-350-841A-1544	Sequence 1544, Ap
31	187	97.4	36	2	US-08-487-266A-5	Sequence 5, Appli
32	187	97.4	36	2	US-09-623-548A-1423	Sequence 1423, Ap
33	187	97.4	36	2	US-10-252-136-5	Sequence 5, Appli
34	187	97.4	36	2	US-09-657-276-1423	Sequence 1423, Ap
35	187	97.4	36	2	US-08-484-741-5	Sequence 5, Appli
36	181	94.3	36	2	US-09-515-965A-1986	Sequence 1986, Ap
37	181	94.3	36	2	US-09-350-641C-1749	Sequence 1749, Ap
38	181	94.3	36	2	US-09-350-841A-1938	Sequence 1938, Ap
39	179	93.2	36	2	US-09-082-279B-642	Sequence 642, App
40	179	93.2	36	2	US-09-315-304B-642	Sequence 642, App
41	179	93.2	36	2	US-09-834-784-642	Sequence 642, App
42	179	93.2	36	2	US-09-515-965A-642	Sequence 642, App
43	179	93.2	36	2	US-09-350-641C-642	Sequence 642, App
44	179	93.2	36	2	US-09-350-841A-642	Sequence 642, App
45	178	92.7	36	2	US-09-082-279B-643	Sequence 643, App

ALIGNMENTS

RESULT 1

US-08-484-223B-240
; Sequence 240, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 240:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-484-223B-240

Query Match 100.0% Score 192; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36

RESULT 2

US-09-082-279B-1360
; Sequence 1360, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1360
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-1360

Query Match 100.0%; Score 192; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36

RESULT 3

US-09-315-304B-1360
; Sequence 1360, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1360
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1360

Query Match 100.0%; Score 192; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36

RESULT 4

US-09-834-784-1360
; Sequence 1360, Application US/09834784
; Patent No. 8562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; PRIOR FILING DATE: 2001-04-13
; CURRENT APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1360
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-1360

Query Match 100.0%; Score 192; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36

RESULT 5

US-09-515-965A-1360
; Sequence 1360, Application US/09515965A
; Patent No. 8623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Siata, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; PRIOR FILING DATE: 2000-02-29
; PRIOR FILING DATE: 1999-05-20
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1360
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-1360

Query Match 100.0%; Score 192; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLEKSIQIQEKNQEELLELDKWSLWNWF 36
Db 1 YTSLIYSLEKSIQIQEKNQEELLELDKWSLWNWF 36	

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RESULT 6
US-09-350-641C-1360
/ Sequence 1360, Application US/09350641C
/ Patent No. 6656906
/ GENERAL INFORMATION:
/ APPLICANT: Barney, S.
/ APPLICANT: Guthrie, K.
/ APPLICANT: Merutka, G.
/ APPLICANT: Anwer, M.
/ APPLICANT: Lambert, D.
/ TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
/ TITLE OF INVENTION: PROPERTIES
/ FILE REFERENCE: 7872-067
/ CURRENT APPLICATION NUMBER: US/09/350,641C
/ CURRENT FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: 09/315,304
/ PRIOR FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: 09/082,279
/ PRIOR FILING DATE: 1998-05-20
/ NUMBER OF SEQ ID NOS: 1757
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1360
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Core polypeptide
US-09-350-641C-1360

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Query Match      100.0%; Score 192; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 YTSLSLLEKSIQOQKNEQELLELDKWSLWNWF 36
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RESULT 7
US-09-350-841A-1360
; Sequence 1360, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1360
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-841A-1360

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Query Match      100.0%; Score 192; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 36: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY
1 YTSIYSLLEKSIQOEKNEQELLELDKWSLWNWF 36
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Db
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RESULT 8
US-09-082-279B-1361
; Sequence 1361, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1361
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide.
US-09-082-279B-1361

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Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Dp 1 YTSIYSLLEKSIQOEKNEQELLELDKWSLWNWF 36

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RESULT 9
US-09-315-304B-1361
; Sequence 1361, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1361
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1361

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Query Match          98.4%; Score 189; DB 2; Length 36;
Best Local Similarity 97.2%; Pred. No. 2.4e-16;
Matches 35: Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy . 1 YTSIYSLLEKSIQQEKNEQELLELDKWSLWNWF 36
 |||||
 Db 1 YTSIYSLLEKSIQQEKNEQELLELDKWSLWNWF 36
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RESULT 10
US-09-834-784-1361

APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,028
FILING DATE: 07-JUN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
US-08-073-028-5

Query Match 97.4%; Score 187; DB 1; Length 36;
Best Local Similarity 97.2%; Pred. No. 4.2e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36

RESULT 15

US-08-486-099-5
Sequence 5, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-5
Query Match 97.4%; Score 187; DB 2; Length 36;
Best Local Similarity 97.2%; Pred. No. 4.2e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36

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Job time : 27.6667 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Perfect score: 192
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	192	100.0	36	3	US-09-809-060-4		Sequence 4, Appli
2	192	100.0	36	4	US-10-351-641-1360		Sequence 1360, Ap
3	192	100.0	36	4	US-10-663-589-40		Sequence 40, Appl
4	192	100.0	36	4	US-10-671-282-40		Sequence 40, Appl
5	192	100.0	36	5	US-10-168-295-5		Sequence 5, Appli
6	192	100.0	36	5	US-10-168-295-57		Sequence 57, Appl
7	189	98.4	36	4	US-10-351-641-1361		Sequence 1361, Ap
8	187	97.4	36	4	US-10-252-138-5		Sequence 5, Appli
9	187	97.4	36	4	US-10-267-682-5		Sequence 5, Appli
10	187	97.4	36	4	US-10-267-748-5		Sequence 5, Appli
11	187	97.4	36	5	US-10-950-010-5		Sequence 5, Appli
12	187	97.4	36	6	US-11-066-697-1423		Sequence 1423, Ap
13	181	94.3	36	4	US-10-351-641-1749		Sequence 1749, Ap
14	179	93.2	36	4	US-10-351-641-642		Sequence 642, App
15	179	93.2	36	4	US-10-457-780-52		Sequence 52, Appl
16	179	93.2	36	5	US-10-950-010-537		Sequence 537, App
17	178	92.7	36	4	US-10-351-641-643		Sequence 643, App
18	178	92.7	36	4	US-09-854-816-112		Sequence 112, App
19	176	91.7	36	5	US-10-950-010-541		Sequence 541, App
20	176	91.7	38	4	US-10-351-641-1509		Sequence 1509, Ap
21	175	91.1	36	4	US-10-351-641-1249		Sequence 1249, Ap
22	175	91.1	36	4	US-10-351-641-1424		Sequence 1424, Ap
23	175	91.1	36	4	US-10-351-641-1751		Sequence 1751, Ap
24	174	90.6	36	3	US-09-809-060-1		Sequence 1, Appli
25	174	90.6	36	3	US-09-809-060-85		Sequence 85, Appl
26	174	90.6	36	3	US-09-796-202-10		Sequence 10, Appl
27	174	90.6	36	3	US-09-960-717-2		Sequence 2, Appli

28	174	90.6	36	3	US-09-779-451-5	Sequence 5, Appl
29	174	90.6	36	3	US-09-834-638-1	Sequence 1, Appl
30	174	90.6	36	3	US-09-828-615-1	Sequence 1, Appl
31	174	90.6	36	3	US-09-854-816-1	Sequence 1, Appl
32	174	90.6	36	3	US-09-854-816-108	Sequence 108, App
33	174	90.6	36	3	US-09-874-475-16	Sequence 16, Appl
34	174	90.6	36	3	US-09-493-346-1	Sequence 1, Appl
35	174	90.6	36	4	US-10-116-797-1	Sequence 1, Appl
36	174	90.6	36	4	US-10-253-136-1	Sequence 1, Appl
37	174	90.6	36	4	US-10-253-136-37	Sequence 37, Appl
38	174	90.6	36	4	US-10-253-136-39	Sequence 39, Appl
39	174	90.6	36	4	US-10-158-742A-8	Sequence 8, Appl
40	174	90.6	36	4	US-10-323-344-10	Sequence 10, Appl
41	174	90.6	36	4	US-10-278-364A-7	Sequence 7, Appl
42	174	90.6	36	4	US-10-351-641-15	Sequence 15, Appl
43	174	90.6	36	4	US-10-351-641-211	Sequence 211, App
44	174	90.6	36	4	US-10-351-641-497	Sequence 497, App
45	174	90.6	36	4	US-10-351-641-498	Sequence 498, App

ALIGNMENTS

```

RESULT 1
US-09-809-060-4
; Sequence 4, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; TITLE OF INVENTION: Regions of HIV Envelope Proteins
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-4

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Query Match      100.0%; Score 132; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYSLLEKSKIQQEKNEQEELLELDKQASLWNWF 36
    | | | | | | | | | | | | | | | | | | | |
Db 1 YTSLIYSLLEKSKIQQEKNEQEELLELDKQASLWNWF 36
    | | | | | | | | | | | | | | | | | | | |

```

```

RESULT 2
US-10-351-641-1360
; Sequence 1360, Application US/10351641
; Publication NO. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; CURRENT APPLICATION NUMBER: 09/315,304

```

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; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1360
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1360

Query Match      100.0%; Score 192; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 3
US-10-663-589-40
; Sequence 40, Application US/10663589
; Publication No. US2004006367A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-40

Query Match      100.0%; Score 192; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 4
US-10-671-282-40
; Sequence 40, Application US/10671282
; Publication No. US20040122214A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
; FILE REFERENCE: TRM-004
; CURRENT APPLICATION NUMBER: US/10/671,282
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/414,439
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: synthesized
US-10-671-282-40

Query Match      100.0%; Score 192; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 5
US-10-168-295-5
; Sequence 5, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Batoudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; OTHER INFORMATION: synthesized
US-10-168-295-5

Query Match      100.0%; Score 192; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 6
US-10-168-295-57
; Sequence 57, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Batoudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; OTHER INFORMATION: synthesized
US-10-168-295-57

Query Match      100.0%; Score 192; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
```

RESULT 7

US-10-351-641-1361
; Sequence 1361, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1361
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1361

Query Match 98.4%; Score 189; DB 4; Length 36;
Best Local Similarity 97.2%; Pred. No. 6.8e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 8

US-10-252-136-5
; Sequence 5, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-5

Query Match 97.4%; Score 187; DB 4; Length 36;
Best Local Similarity 97.2%; Pred. No. 1.2e-14;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 9

US-10-267-682-5
; Sequence 5, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennle & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-267-682-5

Query Match 97.4%; Score 187; DB 4; Length 36;
Best Local Similarity 97.2%; Pred. No. 1.2e-14;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 10

US-10-267-748-5
; Sequence 5, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.


```
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351.641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1749
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1749

Query Match          94.3%; Score 181; DB 4; Length 36;
Best Local Similarity 91.7%; Pred. No. 5,8e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWSLWNWF 36
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Db 1 YTSLIHSLIEESQIQQEKNEQELLELDKWSLWNWF 36

RESULT 14
US-10-351-641-642
; Sequence 642, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351.641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 642
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-642

Query Match          93.2%; Score 179; DB 4; Length 36;
Best Local Similarity 91.7%; Pred. No. 9,9e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWSLWNWF 36
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 YTSLIHSLIEESQIQQEKNEQELLELDKWSLWNWF 36
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RESULT 15
US-10-457-780-52

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; Sequence 52, Application US/10457780
; Publication No. US20040137426A1
; GENERAL INFORMATION:
; APPLICANT: SERRES, Pierre-Francois
; APPLICANT: MOSCA, Joseph
; TITLE OF INVENTION: GP41 PEPTIDES AND METHODS BASED THEREON FOR INHIBITING HIV FUSION
; TITLE OF INVENTION: TO TARGET CELLS
; FILE REFERENCE: 118761
; CURRENT APPLICATION NUMBER: US/10/457,780
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/446,268
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/413,919
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/386,754
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Y36F
US-10-457-780-52

Query Match          93.2%; Score 179; DB 4; Length 36;
Best Local Similarity 91.7%; Pred. No. 9,9e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWSLWNWF 36
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 YTSLIHSLIEESQIQQEKNEQELLELDKWSLWNWF 36

Search completed: March 6, 2006, 15:50:32
Job time : 95 secs
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; APPLICANT: Wesolowski, John
; TITLE OF INVENTION: Fc Fusion Proteins For Enhancing the Immunogenicity of
; TITLE OF INVENTION: Protein and Peptide Antigens
; FILE REFERENCE: LEX-007
; CURRENT APPLICATION NUMBER: US/11/089,426
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US/09/621,268
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/144,965
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fused
; OTHER INFORMATION: polypeptide from pDC-muFC vector
US-11-089-426-10

Query Match      84.4%; Score 162; DB 7; Length 44;
Best Local Similarity 88.2%; Pred. No. 1.8e-14;
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SLIYSLEKSIQIQEKNEQELLELDKWSLWNWF 36
Db 1 SLIHSLEESQIQEKNEQELLELDKWSLWNWF 34

RESULT 7
US-10-506-796A-1
; Sequence 1, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(35)
; OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
US-10-506-796A-1

Query Match      69.8%; Score 134; DB 6; Length 35;
Best Local Similarity 96.0%; Pred. No. 5.2e-11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
Db 1 SQTQEKNEQELLELDKWSLWNWF 25

RESULT 8
US-10-506-796A-3
; Sequence 3, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
```

```
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-506-796A-3

Query Match      69.8%; Score 134; DB 6; Length 36;
Best Local Similarity 96.0%; Pred. No. 5.3e-11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
Db 2 SQTQEKNEQELLELDKWSLWNWF 26

RESULT 9
US-10-841-956A-3
; Sequence 3, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-3

Query Match      68.2%; Score 131; DB 6; Length 39;
Best Local Similarity 75.0%; Pred. No. 1.4e-10;
Matches 24; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 5 IYSLLEKSIQIQEKNEQELLELDKWSLWNWF 36
Db 8 ITALLEQAQIQEKNEVEYELQKLDKWSLWNWF 39

RESULT 10
US-11-029-003-3
; Sequence 3, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEL, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
```


; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: HIV-1 isolate 98BRRS012 (residues 649-685)
US-10-506-796A-6

Query Match 64.6%; Score 124; DB 6; Length 36;
Best Local Similarity 88.0%; Pred. No. 1e-09;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 12 SQIQQKNEQELLELDKWASLWNWF 36
Db 1 SQNQEKNEHELELDKWANLWNWF 25

RESULT 15
US-10-506-796A-4
; Sequence 4, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(35)
; OTHER INFORMATION: HIV-1 isolate MN clone v5 (residues 649-685)
US-10-506-796A-4

Query Match 63.5%; Score 122; DB 6; Length 36;
Best Local Similarity 88.0%; Pred. No. 1.8e-09;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 SQIQQKNEQELLELDKWASLWNWF 36
Db 1 SOTQEKNEQELLELDKWESLWNWF 25

Search completed: March 6, 2006, 15:54:21
Job time : 10 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:12:57 ; Search time 117.333 Seconds
(without alignments)
134.809 Million cell updates/sec

Title: US-09-809-060A-4
Perfect score: 36
Sequence: 1 YTSLLYSLLKSSQIQEKNQELLEDKWSLWNP 36

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	36	3 AAY89840	Aay89840 Core poly
2	36	100.0	36	3 AAY89841	Aay89841 Core poly
3	36	100.0	36	4 AAB78242	Aab78242 Core poly
4	36	100.0	36	4 AAB78241	Aab78241 Core poly
5	36	100.0	36	4 AAU70182	Aau70182 HIV viral
6	36	100.0	36	4 ABB01248	Abb01248 Viral DP1
7	36	100.0	36	4 ABB01249	Abb01249 Viral DP1
8	36	100.0	36	4 ABB02833	Abb02833 Viral cor
9	36	100.0	36	4 AAU13794	Aau13794 DP178-lik
10	36	100.0	36	4 AAU13795	Aau13795 DP178-lik
11	36	100.0	36	5 AAC018774	Aac018774 HIV gp41
12	36	100.0	36	5 AAC018826	Aac018826 HIV gp41
13	36	100.0	36	5 ADE02854	Ades02854 Hybrid po
14	36	100.0	36	5 ADE02853	Ades02853 Hybrid po
15	36	100.0	36	8 ADN06925	Adn06925 Peptide #
16	36	100.0	36	8 ADS87260	Ads87260 HIV-1 gp4
17	36	100.0	36	9 ADY71547	Ady71547 HIV-1 tra
18	36	100.0	36	9 ADY71495	Ady71495 HIV-1 tra
19	25	69.4	36	3 AAY89911	Aay89911 Core poly
20	25	69.4	36	4 AAB78312	Aab78312 Core poly
21	25	69.4	36	4 ABB01319	Abb01319 Viral DP1
22	25	69.4	36	4 AAU13865	Aau13865 DP178-lik
23	25	69.4	36	5 ADE02837	Ades02837 Hybrid po
24	25	69.4	268	2 AAY22811	Aay22811 SEQ ID NO

ALIGNMENTS

RESULT 1

AAy89840
ID AAY89840 standard; peptide; 36 AA.
XX
AC AAY89840;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 1409.
XX
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KW anti-fusogenic; differentiation factor; interleukin; interferon;
KW colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN WO9959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX WPI; 2000-136792/12.
XX
PT A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
XX Disclosure; Page 45; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic

25 25 69.4 268 5 ABG68282 Abg68282 Envelope
26 25 69.4 268 6 ABUS7689 Abus7689 Human Imm
27 25 69.4 269 2 AAY22825 Aay22825 SEQ ID NO
28 25 69.4 269 5 ABG68296 Abg68296 Envelope
29 25 69.4 269 6 ABUS7703 Abus7703 Human Imm
30 25 69.4 848 8 ADP20072 Adp20072 Human Imm
31 25 69.4 848 9 ADX39685 Adx39685 HIV Env p
32 24 66.7 36 4 ABB02834 Aab02834 Viral cor
33 22 61.1 22 2 AAB14657 Aab14657 HIV-1 iso
34 22 61.1 22 3 AAB14657 Aab14657 HIV-1 iso
35 22 61.1 22 3 AAB52674 Aab52674 T20/DP178
36 22 61.1 22 3 AAB52699 Aab52699 T20/DP178
37 22 61.1 22 4 AAB54921 Aab54921 Anti-HIV
38 22 61.1 23 2 AAB64385 Aab64385 DP-178 ho
39 22 61.1 23 3 AAY88708 Aay88708 Core poly
40 22 61.1 23 3 AAB14658 Aab14658 HIV-1 iso
41 22 61.1 23 3 AAB52698 Aab52698 T20/DP178
42 22 61.1 23 3 AAB52675 Aab52675 T20/DP178
43 22 61.1 23 4 AAB54922 Aab54922 Anti-HIV
44 22 61.1 23 4 AAB77063 Aab77063 Core poly
45 22 61.1 23 4 ABB01532 Aab01532 Viral cor

RESULT 4
 ID AAB78241 standard; peptide; 36 AA.
 AC
 XX AAB78241;
 DT
 XX 19-APR-2001 (first entry)
 DE
 XX Core polypeptide T1409.
 KW Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;
 KW antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;
 KW fusion-related disorder; bacterial infection; viral infection.
 XX
 OS Unidentified.
 XX
 XX WO200103723-A1.
 PN
 XX 18-JAN-2001.
 PD
 XX 10-JUL-2000; 2000WO-US018772.
 XX
 XX 09-JUL-1999; 99US-00350641.
 PR
 XX (TRIM-) TRIMERIS INC.
 PA
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 PI
 XX WPI; 2001-147136/15.
 DR
 XX New hybrid polypeptide, useful for preventing, treating and diagnosing
 PT e.g. viral infections, comprises an enhancer peptide linked to a core
 PT polypeptide.
 XX
 PS Disclosure; Page 58; 15ipp; English.
 XX
 CC The present sequence is a core polypeptide which may be linked to an
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to
 CC those exhibited by the core polypeptide when introduced into a living
 CC system. It is used to increase the in vitro or ex vivo half-life of the
 CC core polypeptide. The hybrid and core polypeptides can be used for
 CC modulating fusogenic events and intracellular processes involving coiled-
 CC coil peptide interactions. Other uses include preventing, treating and/or
 CC diagnosing disorders involving fusion events (e.g. modulation of
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral
 CC infections caused by human immunodeficiency virus, respiratory syncytial
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
 CC polio virus). The enhancer peptide sequence increases the half-life and
 CC reduces the clearance rate of therapeutic peptides, which increases their
 CC efficacy and minimises the incidence and severity of adverse side
 CC effects. In addition, this increases the sensitivity of the diagnostic
 CC procedure in which they are used
 XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 36; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 4.2e-25;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36
 Db 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36
 RESULT 5
 AAB78241
 ID AAB78241 standard; peptide; 36 AA.
 XX
 AC AAB78241;
 XX
 DT 11-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 03-JAN-2002 (first entry)

AAU70182;
 14-FEB-2002 (first entry)
 HIV viral envelope protein stabilising peptide #4.
 Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;
 anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
 alpha-helical region; ectodomain.
 Homo sapiens.
 WO200170262-A2.
 27-SEP-2001.
 15-MAR-2001; 2001WO-US008108.
 17-MAR-2000; 2000US-0189981P.
 (PANA-) PANACOS PHARM INC.
 Wild CT, Allaway GP;
 WPI; 2001-626098/72.
 Immunogenic composition for inhibiting HIV infection, comprises viral
 envelope protein or its fragment exterior to viral membrane, a
 stabilizing peptide, and, optionally, viral cell surface receptor or its
 fragment.
 Claim 6; Page 45; 84pp; English.
 The invention relates to methods of generating immunogens that elicit
 neutralising antibodies which target regions of viral envelope proteins
 such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-
 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and
 AAU70677-AAU70743 represent stabilising peptides modelling the alpha-
 helical regions of the ectodomain of the HIV-1 transmembrane protein to
 stabilise fusion-active intermediate structures, which can be used as
 vaccine immunogens. Immunogenic compositions comprise a viral envelope
 protein or its fragment exterior to the viral membrane, a stabilising
 peptide to disrupt formation of structural intermediates necessary for
 viral fusion and entry, and optionally, a viral cell surface receptor or
 its fragment. The stabilising peptide is capable of associating with the
 envelope protein or its fragment to form a stabilised, fusion active
 structure. Antibody binding assays are used to determine the ability of
 immunogen vaccines to generate an immune response to various forms of
 envelope. Virus neutralisation assays can be used to characterise the
 antibody response raised against HIV-1 gp41 domains. The sequences and
 methods are useful for inhibiting HIV infection, for inducing an immune
 response in an animal and for raising antibodies

Query Match 100.0%; Score 36; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 4.2e-25;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36
 Db 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36
 RESULT 6
 ABB01248
 ID ABB01248 standard; peptide; 36 AA.
 XX
 AC ABB01248;
 XX
 DT 11-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 03-JAN-2002 (first entry)

```

XX DE Viral DP178/107-like region peptide T1409.
XX XX
XX KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
XX KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
XX KW infection.
XX OS
XX XX
XX XX Viruses.
XX XX
XX XX Key Location/Qualifiers
XX FT Modified-site 1
XX FT Modified-site 36 /note= "N-terminal is substituted by Ac"
XX FT Modified-site 36 /note= "C-terminal amide"
XX XX
XX XX WO200164013-A2.
XX XX
XX PD 07-SEP-2001.
XX XX
XX XX 07-FEB-2001; 2001WO-US003988.
XX XX
XX XX 29-FEB-2000; 2000US-00515965.
XX XX
XX XX (TRIM-) TRIMERIS INC.
XX XX
XX XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX XX WPI; 2001-514829/56.
XX XX
XX XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
XX XX fusion, useful for treating HIV and Respiratory Syncytial Virus
XX XX infection.
XX XX
XX XX Disclosure; Page 58; 587pp; English.
XX XX
XX XX The invention relates to isolated analogues of the heptad repeat region
XX XX peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
XX XX 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
XX XX respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
XX XX regions of proteins interact non-covalently with each other and/or with
XX XX peptides derived from them. This interaction is required for normal
XX XX infectivity of viruses such as RSV and HIV. The heptad repeat region
XX XX peptide analogues may be used to inhibit respiratory syncytial virus
XX XX (RSV) infection in a cell. They may also be used to inhibit HIV
XX XX infection. The present sequence is a peptide provided in the
XX XX specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
XX XX 11-SEP-2003 to standardise OS field)
XX XX
XX SQ Sequence 36 AA;
XX
XX Query Match 100.0%; Score 36; DB 4; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-25;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 YTSLIYSLLKESQIQQEKNEQLLELDKWASLWNWF 36
XX | | | | | | | | | | | | | | | | | | | | | |
XX Db 1 YTSLIYSLLKESQIQQEKNEQLLELDKWASLWNWF 36
XX | | | | | | | | | | | | | | | | | | | | | |
XX
XX RESULT 7
XX ABB01249
XX ID ABB01249 standard; peptide; 36 AA.
XX XX
XX AC ABB01249;
XX XX
XX XX 11-SEP-2003 (revised)
XX DT 06-AUG-2003 (revised)
XX DT 03-JAN-2002 (first entry)
XX XX
XX XX Viral DP178/107-like region peptide T1410.
XX XX
XX XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
XX KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;

```

```

KW infection.
XX XX
XX OS Viruses.
XX XX
XX PN WO200164013-A2.
XX XX
XX XX PD 07-SEP-2001.
XX XX
XX XX 07-FEB-2001; 2001WO-US003988.
XX XX
XX PR 29-FEB-2000; 2000US-00515965.
XX XX
XX PA (TRIM-) TRIMERIS INC.
XX XX
XX PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX XX WPI; 2001-514829/56.
XX XX
XX DR Heptad repeat region peptide analogs useful for inhibiting virus/cells
XX XX fusion, useful for treating HIV and Respiratory Syncytial Virus
XX XX infection.
XX XX
XX PS Disclosure; Page 58; 587pp; English.
XX XX
XX CC The invention relates to isolated analogues of the heptad repeat region
XX CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
XX CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
XX CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
XX CC regions of proteins interact non-covalently with each other and/or with
XX CC peptides derived from them. This interaction is required for normal
XX CC infectivity of viruses such as RSV and HIV. The heptad repeat region
XX CC peptide analogues may be used to inhibit respiratory syncytial virus
XX CC (RSV) infection in a cell. They may also be used to inhibit HIV
XX CC infection. The present sequence is a peptide provided in the
XX CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
XX CC 11-SEP-2003 to standardise OS field)
XX CC
XX SQ Sequence 36 AA;
XX
XX Query Match 100.0%; Score 36; DB 4; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-25;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 YTSLIYSLLKESQIQQEKNEQLLELDKWASLWNWF 36
XX | | | | | | | | | | | | | | | | | | | | | |
XX Db 1 YTSLIYSLLKESQIQQEKNEQLLELDKWASLWNWF 36
XX | | | | | | | | | | | | | | | | | | | | | |
XX
XX RESULT 8
XX ABB02833
XX ID ABB02833 standard; peptide; 36 AA.
XX XX
XX AC ABB02833;
XX XX
XX DT 11-SEP-2003 (revised)
XX DT 06-AUG-2003 (revised)
XX DT 03-JAN-2002 (first entry)
XX XX
XX DE Viral core polypeptide, SEQ ID NO: 1360.
XX XX
XX XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
XX KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
XX KW infection.
XX XX
XX OS Viruses.
XX XX
XX PN WO200164013-A2.
XX XX
XX PD 07-SEP-2001.
XX XX
XX PF 07-FEB-2001; 2001WO-US003988.
XX XX
XX PR 29-FEB-2000; 2000US-00515965.

```


CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antifusogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents one of the DP178-like/DP107-like peptides of the invention
 XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 4.2e-25;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
 |||||
 Db 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 11

AAO18774
 ID AAO18774 standard; peptide; 36 AA.

AC AAO18774;

XX 29-OCT-2002 (first entry)

DE HIV gp41 protein DP-178 region derived peptide SEQ ID NO: 5.

XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
 KW gp41.

XX Human immunodeficiency virus.

OS WO200256902-A2.

XX 25-JUL-2002.

XX 17-DEC-2001; 2001WO-US048802.

XX 19-DEC-2000; 2000US-0256657P.

XX (SCHE) SCHERING CORP.

XX Baroudy BM;

XX WPI; 2002-636513/68.

XX Treatment of HIV infection in an individual involves administration of a
 PT combination of chemokine co-receptor five antagonist and a specified HIV
 PT envelope polypeptide.

XX Disclosure; Page 32; 52pp; English.

XX The present invention relates to a method of treating an HIV infection in
 CC an individual, which involves administering in combination a chemokine co
 CC -receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
 CC derivative. Other viral infections can also be treated using the method.
 CC The present sequence is a peptide derived from HIV and useful in the
 CC method of the invention

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 5; Length 36;
 Best Local Similarity 100.0%; Pred. No. 4.2e-25;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
 |||||
 Db 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 12

AAO18826
 ID AAO18826 standard; peptide; 36 AA.

XX AAO18826;

XX 29-OCT-2002 (first entry)

DE HIV gp41 protein DP-178 region derived peptide SEQ ID NO: 57.

XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;
 KW gp41.

XX Human immunodeficiency virus.

XX WO200256902-A2.

XX 25-JUL-2002.

XX 17-DEC-2001; 2001WO-US048802.

XX 19-DEC-2000; 2000US-0256657P.

XX (SCHE) SCHERING CORP.

XX Baroudy BM;

XX WPI; 2002-636513/68.

XX Treatment of HIV infection in an individual involves administration of a
 PT combination of chemokine co-receptor five antagonist and a specified HIV
 PT envelope polypeptide.

XX Disclosure; Page 34; 52pp; English.

XX The present invention relates to a method of treating an HIV infection in
 CC an individual, which involves administering in combination a chemokine co
 CC -receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its
 CC derivative. Other viral infections can also be treated using the method.
 CC The present sequence is a peptide derived from HIV and useful in the
 CC method of the invention

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 5; Length 36;
 Best Local Similarity 100.0%; Pred. No. 4.2e-25;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
 |||||
 Db 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 13

ADE02854
 ID ADE02854 standard; peptide; 36 AA.

XX ADE02854;

XX 29-JAN-2004 (first entry)

DE Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID NO 1361.

XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;
 KW pharmacokinetic; fusogenic; insulin; diabetes.

OS Unidentified.
XX US6348568-B1.
XX
XX
PD 19-FEB-2002.
XX
XX
PF 20-MAY-1999; 99US-00315304.
XX
XX
PR 20-MAY-1998; 98US-00082279.
XX
XX
XX (TRIM-) TRIMERIS INC.
XX
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
XX WPI; 2002-424396/45.
XX
XX
XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral
XX activity, has enhancer peptide sequence derived from retroviral envelope
XX protein sequences linked to core polypeptide e.g. therapeutic protein.
XX
XX
XX Disclosure; SEQ ID NO 1361; 70pp; English.
XX
XX
XX The invention relates to a novel hybrid polypeptide comprising an
XX enhancer peptide sequence linked to a core polypeptide. The enhancer
XX peptide sequence comprises WQWEQKI or WASLWFW. The invention also
XX includes novel peptides that exhibit anti-fusogenic activity, antiviral
XX activity and/or ability to modulate intracellular processes. The novel
XX hybrid polypeptide has virucide and antidiabetic activity. The enhancer
XX peptide sequence enhances pharmacokinetic properties of any core
XX polypeptide, for example, a polypeptide useful for the treatment or
XX prevention of a disease, or an imaging agent useful for imaging
XX structures in vivo. The core polypeptides and hybrid polypeptides are
XX useful for modulating fusogenic events and exhibit antifusogenic or
XX antiviral activity. The novel hybrid polypeptide is useful for decreasing
XX viral infection and modulating intracellular processes involving coiled-
XX coil peptide interactions. The novel hybrid polypeptide comprises insulin
XX or its fragment, so the core polypeptide is useful for ameliorating the
XX symptoms of forms of diabetes. The novel hybrid polypeptide is also
XX useful as a part of prognosis for preventing disorders including fusion
XX events and viral infection that involves cell-cell and/or virus-cell
XX fusion, and for diagnosis and in vivo imaging methods. This sequence
XX represents an enhancer peptide of the invention.
XX
XX
SQ Sequence 36 AA;
Query Match 100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.2e-25;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTSLIYSLEKSIQIQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLEKSIQIQEKNEQELLELDKWASLWNWF 36
RESULT 14
ADE02853
ID ADE02853 standard; peptide; 36 AA.
XX
XX ADE02853;
XX
XX 29-JAN-2004 (first entry)
XX
XX Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID NO 1360.
XX
XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;
XX pharmacokinetic; fusogenic; insulin; diabetes.
XX
XX Unidentified.
XX
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note= "Residue is modified by acetyl group"
XX Modified-site 36

/note= "C-terminal amide"
FT US6348568-B1.
XX
XX
XX 19-FEB-2002.
XX
XX
XX 20-MAY-1999; 99US-00315304.
XX
XX
XX 20-MAY-1998; 98US-00082279.
XX
XX
XX (TRIM-) TRIMERIS INC.
XX
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
XX WPI; 2002-424396/45.
XX
XX
XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral
XX activity, has enhancer peptide sequence derived from retroviral envelope
XX protein sequences linked to core polypeptide e.g. therapeutic protein.
XX
XX
XX Disclosure; SEQ ID NO 1360; 70pp; English.
XX
XX
XX The invention relates to a novel hybrid polypeptide comprising an
XX enhancer peptide sequence linked to a core polypeptide. The enhancer
XX peptide sequence comprises WQWEQKI or WASLWFW. The invention also
XX includes novel peptides that exhibit anti-fusogenic activity, antiviral
XX activity and/or ability to modulate intracellular processes. The novel
XX hybrid polypeptide has virucide and antidiabetic activity. The enhancer
XX peptide sequence enhances pharmacokinetic properties of any core
XX polypeptide, for example, a polypeptide useful for the treatment or
XX prevention of a disease, or an imaging agent useful for imaging
XX structures in vivo. The core polypeptides and hybrid polypeptides are
XX useful for modulating fusogenic events and exhibit antifusogenic or
XX antiviral activity. The novel hybrid polypeptide is useful for decreasing
XX viral infection and modulating intracellular processes involving coiled-
XX coil peptide interactions. The novel hybrid polypeptide comprises insulin
XX or its fragment, so the core polypeptide is useful for ameliorating the
XX symptoms of forms of diabetes. The novel hybrid polypeptide is also
XX useful as a part of prognosis for preventing disorders including fusion
XX events and viral infection that involves cell-cell and/or virus-cell
XX fusion, and for diagnosis and in vivo imaging methods. This sequence
XX represents an enhancer peptide of the invention.
XX
XX
SQ Sequence 36 AA;
Query Match 100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.2e-25;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTSLIYSLEKSIQIQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLEKSIQIQEKNEQELLELDKWASLWNWF 36
RESULT 15
ADN06925
ID ADN06925 standard; protein; 36 AA.
XX
XX ADN06925;
XX
XX 17-JUN-2004 (first entry)
XX
XX Peptide #36 used in the pharmaceutical composition of the invention.
XX
XX Pharmaceutical; human immunodeficiency virus; HIV; gp41; glycoprotein41;
XX HIV infection; antiviral; therapy.
XX
XX Unidentified.
XX
XX
XX US2004063637-A1.
XX
XX 01-APR-2004.
XX

PF 16-SEP-2003; 2003US-00663589.
XX
PR 27-SEP-2002; 2002US-0414441P.
XX
XX (HEIL/) HEILMAN D.
PA (DIJJ/) DI J.
PA (BRAY/) BRAY B.
XX
PI Heilman D, Di J, Bray B;
XX
DR WPI; 2004-339372/31.
XX
PT Pharmaceutical composition used to treat Human Immunodeficiency Virus
PT comprises solution comprising synthetic peptide (Human Immunodeficiency
PT Virus fusion inhibitor) in mixture with polyol.
XX
PS Disclosure; SEQ ID NO 40; 36pp; English.
XX
CC The present invention relates to a pharmaceutical composition comprised
CC of polymer admixed with synthetic peptides derived from human
CC immunodeficiency virus (HIV) gp41. The invention is useful in treating
CC HIV infection (preferably HIV-1) and act as antiviral agent. The
CC present sequence is a peptide used in the pharmaceutical composition of
CC the invention
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 8; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.2e-25;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIYSLEKSOIQOEKNEQELLELDKWASLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |
DB 1 YTSLIYSLEKSOIQOEKNEQELLELDKWASLWNWF 36
| | | | | | | | | | | | | | | | | | | | | |

Search completed: March 6, 2006, 16:19:05
Job time : 117.333 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:19:28 ; Search time 19 Seconds
(without alignments)
182.305 Million cell updates/sec

Title: US-09-809-060A-4
Perfect score: 36
Sequence: 1 YTSLLVLEKSIQKEKNEQELLELDKWASLWNWF 36

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	61.1	357	2 S21994	envelope protein g
2	22	61.1	357	2 S21996	envelope protein g
3	22	61.1	358	2 S21998	envelope protein g
4	22	61.1	443	2 C41621	env polypeptide P
5	22	61.1	847	2 T09448	envelope glycoprotein
6	22	61.1	847	2 S13289	env protein - huma
7	22	61.1	851	2 S33985	env polypeptide -
8	22	61.1	853	2 S54384	envelope polypeptide
9	22	61.1	854	2 S13288	env protein - huma
10	22	61.1	855	1 VCLJ32	env polypeptide pr
11	22	61.1	855	1 VCLJ2R	env polypeptide pr
12	22	61.1	856	1 VCLJ3W	env polypeptide pr
13	22	61.1	856	1 VCLJH3	env polypeptide pr
14	22	61.1	859	1 VCLJWN	env polypeptide pr
15	22	61.1	861	1 VCLJSC	env polypeptide pr
16	22	61.1	861	1 VCLJ3V	env polypeptide pr
17	19	52.8	357	2 S21992	envelope protein g
18	16	44.4	852	2 T12016	envelope glycoprotein
19	16	44.4	856	1 VCLJVL	env polypeptide pr
20	15	41.7	846	1 VCLJND	env polypeptide pr
21	15	41.7	852	1 VCLJBR	env polypeptide -
22	15	41.7	859	2 T01672	envelope polypeptide
23	11	30.6	445	2 A41621	env polypeptide M
24	11	30.6	843	1 H44001	env polypeptide pr
25	10	27.8	357	2 S22004	envelope protein g
26	10	27.8	357	2 S22006	envelope protein g
27	10	27.8	357	2 S21990	envelope protein g
28	8	22.2	454	2 B41621	env polypeptide D
29	8	22.2	592	2 T03682	catechol oxidase (

30 catechol oxidase (

31 catechol oxidase (

32 env polypeptide pr

33 env polypeptide -

34 envelope polypeptide

35 envelope polypeptide

36 env protein - huma

37 env protein - huma

38 env protein - huma

39 env protein - huma

40 env protein - huma

41 env protein - huma

42 env protein - huma

43 env protein - huma

44 env protein - huma

45 env protein - huma

ALIGNMENTS

RESULT 1

S21994

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

A;Variety: isolate 27B

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S21994; S70421

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A;Reference number: S21990

A;Accession: S21994

A;Molecule type: DNA

A;Residues: 1-357 <STE1>

A;Cross-references: UNIPROT:Q78118; UNIPARC:UPI0000178606; EMBL:X61355; NID:G60179; PIDN

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr

A;Reference number: S70417; MUID:92144209; PMID:1736940

A;Accession: S70421

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>

A;Cross-references: UNIPARC:UPI00000FF05F; EMBL:X61355; NID:G60179

C;Superfamily: type E retrovirus env polypeptide

Query Match 61.1%; Score 22; DB 2; Length 357;

Best Local Similarity 100.0%; Pred. No. 4.6e-14;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QQEKNEQELLELDKWASLWNWF 36

Db 153 QQEKNEQELLELDKWASLWNWF 174

RESULT 2

S21996

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S70422; S21996

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr

A;Reference number: S70417; MUID:92144209; PMID:1736940

A;Accession: S70422

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-357 <ST2>

A;Cross-references: UNIPROT:Q78119; UNIPARC:UPI0000104EC6; EMBL:X61356; NID:G60181; PIDN

A;Experimental source: patient 27L

A;Note: submitted to the EMBL Data Library, July 1991

C;Superfamily: type E retrovirus env polyprotein

```
Query Match      61.1%; Score 22; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 4.6e-14;
Matches 22; Conservative 0; Mismatches 0; Indels
```

Qy 15 QOEKNEQELLELDKWASLWNWF 36
153 QOEKNEQELLELDKWASLWNWF 174
Db

RESULT 3

S21998
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 28
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S21998; S70425
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by polymerase chain reaction (PCR) and sequencing
A;Reference number: S21990
A;Accession: S21998
A;Molecule type: DNA
A;Residues: 1-358 <STEL>
A;Cross-references: UNIPROT:Q78120; UNIPARC:UPI0000178607; EMBL:X61359; NID:g60182; PIDN:G60182
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction (PCR) and sequencing
A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70425
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-222, 'X', 224-358 <ST82>
A;Cross-references: UNIPARC:UPI00000FE72C; EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PIDN:CAA43630.1; PIDN:CAA43630.1
C;Superfamily: type E retrovirus env polyprotein

```
Query Match      61.1%; Score 22; DB 2; Length 358;
Best Local Similarity 100.0%; Pred.No. 4.6e-14;
Matches 22; Conservative 0; Mismatches 0; Indels
```

Qy	15	QOEKNEQELLELDKWASLWNWF	36
Db	154	QOEKNEQELLELDKWASLWNWF	179

RESULT 4

C41621
env polypolyprotein P - human immunodeficiency virus type 1 (fragment)
N/Alternate names: coat polypolyprotein
N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: C41621
N/Burger, H.; Weisner, B.; Flaherty, K.; Gullia, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A/Reference number: A41621; MUID:92107924; PMID:11763038
A/Accession: C41621
A/Molecule type: DNA
A/Residues: 1-443 <BUR>
A/Cross-references: UNIPROT:Q80023; UNIPARC:UPI0000104256; GB:M77230; NID:G328631; PIDN:
A/Note: this virus was isolated from the mother's sexual partner
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polypolyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F/1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F/252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F/424-443/Domain: transmembrane #status predicted <TM>
F/424-723/Length: 107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 61.1%; Score 22; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
Matches 22; Conservative 0; Mismatches 0; Indels

QY 15 QOEKNEQELLELDKQASLWNWF 36
db 392 QOEKNEQELLELDKQASLWNWF 413

RESULT 5

T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09448
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI000010C516; EMBL:U63632; NID:g1465777; PI
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match 61.1%; Score 22; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels

QY 15 QQEKNEQELLELDKQWASLWNWF 36
Ddb 643 QQEKNEQELLELDKQWASLWNWF 664

RESULT 6

S13289
env protein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S13289
R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, Nature 346, 69-73, 1990
A/Title: HIV-1 tropism for mononuclear phagocytes can be determined by resistin
A/Reference number: S13288; PMID:91043044; PMID:2172833
A/Accession: S13289
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-847 <OBR>
A/Cross-references: UNIPROT:Q75760; UNIPARC:UPI000017861B
C/Superfamily: type E retrovirus env polypovrotein

Query Match 61.1%; Score 22; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels

QY 15 QOEKNEQELLELDKWASLWNWF 36
| | | | |
Db 643 OOEKNEOELLELDKWASLWNWF 664

RESULT 7

S33985
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S33985
R:Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A>Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-851 <R>
A:Cross-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:Z11530; NID:G60192; PIDN
C:Superfamily: type E retrovirus env polyprotein

Query Match 61.1%; Score 22; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QOEKNEQELLELDKWASLWNWF 36
DB 647 QOEKNEQELLELDKWASLWNWF 668

RESULT 8
S54384
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S54384
R:Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <T>
A:Cross-references: UNIPROT:P12487; UNIPARC:UPI000012A027; EMBL:M22639; NID:G329377; PID
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: polyprotein

Query Match 61.1%; Score 22; DB 2; Length 853;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QOEKNEQELLELDKWASLWNWF 36
DB 649 QOEKNEQELLELDKWASLWNWF 670

RESULT 9
S13288
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C:Accession: S13288
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Digne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <R>
A:Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:Q90178; UNIPROT:Q78243; UNIP

Query Match 61.1%; Score 22; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QOEKNEQELLELDKWASLWNWF 36
DB 650 QOEKNEQELLELDKWASLWNWF 671

RESULT 10
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03976

R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sh
Science 227, 484-492, 1985
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A:Reference number: A04003; MUID:85090453; PMID:2578227
A:Accession: A03976
A:Molecule type: DNA
A:Residues: 1-855 <S>
A:Cross-references: UNIPROT:P03378; UNIPARC:UPI000012A00F; GB:K02007; NID:G328658; PIDN:
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TMM>
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,445,458
F:610,624,636,815/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 61.1%; Score 22; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QOEKNEQELLELDKWASLWNWF 36
DB 651 QOEKNEQELLELDKWASLWNWF 672

RESULT 11
VCLJ3R
env polyprotein precursor - human immunodeficiency virus Zr-6
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus Zr-6
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: D26192
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti
A:Reference number: A26192; MUID:87248097; PMID:3036660
A:Accession: D26192
A:Molecule type: DNA
A:Residues: 1-855 <SRI>
A:Cross-references: UNIPROT:P04580; UNIPARC:UPI000012A029; GB:K03458; NID:G32
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-855/Product: env polyprotein #status predicted <MAT>
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TMM>
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 61.1%; Score 22; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 QOEKNEQELLELDKWASLWNWF 36
DB 651 QOEKNEQELLELDKWASLWNWF 672

RESULT 12
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: A24774
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the en
A:Reference number: A24774; MUID:86218077; PMID:2423250
A:Accession: A24774

```
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: UNIPROT:P31872; UNIPARC:UPI000012A024; GB:M38432; NID:919
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp120 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459
Query Match 61.1%; Score 22; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 652 QOEKNEQELLELDKWASLWNWF 673

RESULT 13
VCLJH3
env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doranberger, J.A.; Papas, T.S.; Grzyb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:8511123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K0200
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMW>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 61.1%; Score 22; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 652 QOEKNEQELLELDKWASLWNWF 673

RESULT 14
VCLJMN
env polypeptide precursor - human immunodeficiency virus type 1 (isolate MN)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: A28922
R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staal
Virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: A28922
A:Molecule type: DNA
A:Residues: 1-859 <GUR>
A:Cross-references: UNIPARC:UPI0000174A38
```

```
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-859/Product: env polypeptide #status predicted <PPP>
F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401
Query Match 61.1%; Score 22; DB 1; Length 859;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 656 QOEKNEQELLELDKWASLWNWF 677

RESULT 15
VCLJSC
env polypeptide precursor - human immunodeficiency virus type 1 (isolate SC)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: B28922
R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staal
Virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>
A:Cross-references: UNIPARC:UPI0000174A39
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-861/Product: env polypeptide #status predicted <PPP>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396
Query Match 61.1%; Score 22; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 657 QOEKNEQELLELDKWASLWNWF 678

Search completed: March 6, 2006, 16:26:19
Job time : 19 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:13:17 ; Search time 122 Seconds
(without alignments)
208.189 Million cell updates/sec

Title: US-09-809-060A-4
Perfect score: 36
Sequence: 1 YTSLLYSLLEKSIQOEKNEQELLELDKWSLWVWF 36

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	80.6	121	2 Q6WH74_9HIV1	Q6wh74 human immun
2	29	80.6	122	2 Q9EA81_9HIV1	Q9ea81 human immun
3	29	80.6	122	2 Q9YXQ1_9HIV1	Q9yxq1 human immun
4	27	75.0	122	2 Q6DL64_9HIV1	Q6dl64 human immun
5	27	75.0	128	2 Q6JEV9_9HIV1	Q6jev9 human immun
6	27	75.0	145	2 Q7ZCS5_9HIV1	Q7zcs5 human immun
7	27	75.0	146	2 Q6JFV9_9HIV1	Q6jfv9 human immun
8	27	75.0	867	2 Q7ZC00_9HIV1	Q7zc00 human immun
9	27	75.0	868	2 Q7ZC01_9HIV1	Q7zc01 human immun
10	26	72.2	126	2 Q6V908_9HIV1	Q6v908 human immun
11	25	69.4	34	2 Q69893_9HIV1	Q69893 human immun
12	25	69.4	49	2 Q69895_9HIV1	Q69895 human immun
13	25	69.4	49	2 Q69896_9HIV1	Q69896 human immun
14	25	69.4	118	2 Q9E583_9HIV1	Q9e583 human immun
15	25	69.4	121	2 Q6WH14_9HIV1	Q6wh14 human immun
16	25	69.4	122	2 Q6WG09_9HIV1	Q6wg09 human immun
17	25	69.4	122	2 Q6WH11_9HIV1	Q6wh11 human immun
18	25	69.4	122	2 Q6DL06_9HIV1	Q6dl06 human immun
19	25	69.4	122	2 Q6DL34_9HIV1	Q6dl34 human immun
20	25	69.4	122	2 Q6DL40_9HIV1	Q6dl40 human immun
21	25	69.4	122	2 Q9EA80_9HIV1	Q9ea80 human immun
22	25	69.4	125	2 Q6V900_9HIV1	Q6v900 human immun
23	25	69.4	130	2 Q6V823_9HIV1	Q6v823 human immun
24	25	69.4	142	2 Q6JFE1_9HIV1	Q6jfe1 human immun
25	25	69.4	144	2 Q7ZC91_9HIV1	Q7zc91 human immun
26	25	69.4	144	2 Q6JFJ2_9HIV1	Q6jfj2 human immun
27	25	69.4	724	2 Q9QKH4_9HIV1	Q9qkh4 human immun
28	25	69.4	831	2 Q6S516_9HIV1	Q6s516 human immun
29	25	69.4	848	1 ENV_HV1JR	P20871 human immun
30	25	69.4	848	2 Q6BC22_9HIV1	Q6bc22 human immun
31	25	69.4	848	2 Q6TAN0_9HIV1	Q6tan0 human immun

32	25	69.4	848	2 Q6TAN1_9HIV1	Q6tan1 human immun
33	25	69.4	848	2 Q6TAN2_9HIV1	Q6tan2 human immun
34	25	69.4	848	2 Q74999_9HIV1	Q74999 human immun
35	25	69.4	850	2 Q79795_9HIV1	Q79795 human immun
36	25	69.4	855	2 Q902H5_9HIV1	Q902h5 human immun
37	25	69.4	860	2 Q41532_9HIV1	Q41532 human immun
38	25	69.4	868	2 Q8Q861_9HIV1	Q8q861 human immun
39	22	61.1	34	2 Q69894_9HIV1	Q69894 human immun
40	22	61.1	34	2 Q69905_9HIV1	Q69905 human immun
41	22	61.1	42	2 Q69910_9HIV1	Q69910 human immun
42	22	61.1	49	2 Q69909_9HIV1	Q69909 human immun
43	22	61.1	117	2 Q6WH02_9HIV1	Q6wh02 human immun
44	22	61.1	117	2 Q6WH53_9HIV1	Q6wh53 human immun
45	22	61.1	117	2 Q6WH80_9HIV1	Q6wh80 human immun

ALIGNMENTS

RESULT 1
Q6WH74_9HIV1
ID Q6WH74_9HIV1 PRELIMINARY; PRT; 121 AA.
AC Q6WH74;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX PubMed=14715797; DOI=10.1128/JCM.42.1.426-430.2004;
RA Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,
RA Gouvea M.I.F.S., Guimaraes M.A.A.M., De Oliveira F.E.,
RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;
RT "Prevalence of human immunodeficiency virus drug resistance mutations and subtypes in drug-naive, infected individuals in the army health service of Rio de Janeiro, Brazil."
RL J. Clin. Microbiol. 42:426-430(2004).
DR EMBL; AY285022; AAQ68085.1; -; Genomic RNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1 121
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 14738 MW; 65B8CB4D6200BFAF CRC64;
Query Match 80.6%; Score 29; DB 2; Length 121;
Best Local Similarity 100.0%; Pred.No. 6.9e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 LLEKSIQOEKNEQELLELDKWSLWVWF 36
Db 84 LLEKSIQOEKNEQELLELDKWSLWVWF 112
RESULT 2
Q9EA81_9HIV1
ID Q9EA81_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q9EA81;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

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OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BX923;
RX MEDLINE=20134570; PubMed=10669328; DOI=10.1086/315253;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475 (2000).
DR EMBL; AF190971; AAG02333.1; -; Genomic_DNA.
DR HSSP; P12488; 11W7.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Name=env;
DR Envelope protein.
DR NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14753 MW; C3FE4DB1F8B5BCBD CRC64;

Query Match 80.6%; Score 29; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.9e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LLEKSQIQEQKNEQELLELDKWSLWNWF 36
Db 85 LLEKSQIQEQKNEQELLELDKWSLWNWF 113

RESULT 3
Q9YXQ1_9HIV1
ID Q9YXQ1_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q9YXQ1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99125811; PubMed=9928731;
RA Tanuri A., Swanson P., Devare S., Berro O.J., Savedra A., Costa L.J.,
RA Telles J.G., Brindeiro R., Schable C., Pieniazek D., Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 20:60-66 (1999).
DR EMBL; AF034052; AAC79304.1; -; Genomic_RNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Name=env;
DR Envelope protein.
DR NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14792 MW; 75BBB60146B8FD17 CRC64;

Query Match 80.6%; Score 29; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.9e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LLEKSQIQEQKNEQELLELDKWSLWNWF 36
Db 85 LLEKSQIQEQKNEQELLELDKWSLWNWF 113

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RESULT 4
Q6DL64_9HIV1
ID Q6DL64_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q6DL64;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kalish M.L., Robbins K.E., Pieniazek D., Schaefer A., Nzilambi N.,
RA Quinn T.C., StLouis M.E., Youngpairoj A.S., Phillips J., Jaffe H.W.,
RA Folks T.M.;
RT "Recombinant viruses and early global HIV-1 epidemic.";
RL Emerg. Infect. Dis. 10:1227-1234 (2004).
DR EMBL; AY667639; AAT74945.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Name=env;
DR Envelope protein.
DR NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14800 MW; 862308FF35EB4A3F CRC64;

Query Match 75.0%; Score 27; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 5.7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EKSQIQEQKNEQELLELDKWSLWNWF 36
Db 87 EKSQIQEQKNEQELLELDKWSLWNWF 113

RESULT 5
Q6JEV9_9HIV1
ID Q6JEV9_9HIV1 PRELIMINARY; PRT; 128 AA.
AC Q6JEV9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang C., Li M., Shi Y.P., Winter J., van Bijik A.M., Ayisi J., Hu D.J.,
RA Steketee R., Nahlen B.L., Lal R.B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY493156; AAT05980.1; -; Genomic_RNA.
DR SMR; O6JEV9; 1-74.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Name=env;
DR Envelope protein.
DR NON_TER 1 1
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 15494 MW; 807346D5EB52C194 CRC64;

Query Match 75.0%; Score 27; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.9e-18;

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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EKSQIQEKNEQELLELDKWSLWNWF 36
    |||||
Db 95 EKSQIQEKNEQELLELDKWSLWNWF 121

RESULT 6
Q7ZC55_9HIV1 PRELIMINARY; PRT; 145 AA.
AC Q7ZC55;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22679027; PubMed=12794544;
RX DOI=10.1097/00126334-200306010-00003;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1 strains."
RL J. Acquir. Immune Defic. Syndr. 33:134-139(2003).
DR EMBL; AY185465; AA065740.1; -; Genomic_RNA.
DR HSSP; P04578; 1DLB.
DR SMR; Q7ZC55; 9-92.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16928 MW; D72B68F6A0812805 CRC64;

Query Match 75.0%; Score 27; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 6.6e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EKSQIQEKNEQELLELDKWSLWNWF 36
    |||||
Db 116 EKSQIQEKNEQELLELDKWSLWNWF 142

RESULT 7
Q6JFV9_9HIV1 PRELIMINARY; PRT; 146 AA.
AC Q6JFV9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Yang C., Li M., Shi Y.P., Winter J., van Eijk A.M., Ayisi J., Hu D.J.,
RA Steketee R., Nahlen B.L., Lal R.B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY492806; AAT05630.1; -; Genomic_RNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6JFV9; 1-82.
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DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 17524 MW; 642595EF4695BB02 CRC64;

Query Match 75.0%; Score 27; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 6.6e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EKSQIQEKNEQELLELDKWSLWNWF 36
    |||||
Db 103 EKSQIQEKNEQELLELDKWSLWNWF 129

RESULT 8
Q7ZC00_9HIV1 PRELIMINARY; PRT; 867 AA.
AC Q7ZC00;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein.
GN Name=gp160;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Daniela R.S., Wilson P., Patel D., Longhurst H., Patterson S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AJ535609; CAD59656.1; -; Genomic_DNA.
DR HSSP; P04578; 1DLB.
DR SMR; Q7ZC00; 83-127, 209-503, 551-637.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 867 AA; 98421 MW; 7FAA0669D0649A14 CRC64;

Query Match 75.0%; Score 27; DB 2; Length 867;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EKSQIQEKNEQELLELDKWSLWNWF 36
    |||||
Db 658 EKSQIQEKNEQELLELDKWSLWNWF 684

RESULT 9
Q7ZC01_9HIV1 PRELIMINARY; PRT; 868 AA.
AC Q7ZC01;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein.
GN Name=gp160;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RA Daniels R.S., Wilson P., Patel D., Longhurst H., Patterson S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535608; CAD59655.1; -; Genomic_DNA.
DR HSSP; P04578; 1DLB.
DR SMR; Q72C01; 83-127, 209-504, 552-638.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR InterPro; IPR000777; Gp120.
DR Pfam; PF00516; Gp120; 1.
DR Pfam; PF00517; Gp41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 868 AA; 98437 MW; F563775C680E2348 CRC64;

Query Match 75.0%; Score 27; DB 2; Length 869;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EKSQIQEKNEQELLELDKWSLWNWF 36
Db 659 EKSQIQEKNEQELLELDKWSLWNWF 685

RESULT 10
ID Q6V908_9HIV1 PRELIMINARY; PRT; 126 AA.
AC Q6V908;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yilmaz G., Midilli K., Turkoglu S., Kuskucu A.M., Bayraktaroglu Z.,
RA Aksozek A., Ozkan E., Calangu S., Altas K.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347721; AAQ63656.1; -; Genomic_DNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; Gp41; 1.
KW Envelope protein.
FT NON_TER 1 126
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 15130 MW; 7F9C6AEB08ADE84C CRC64;

Query Match 72.2%; Score 26; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 5.3e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LLEKSQIQEKNEQELLELDKWSLW 33
Db 89 LLEKSQIQEKNEQELLELDKWSLW 114

RESULT 11
Q69893_9HIV1
ID Q69893_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

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OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06723; AAA19136.1; -; mRNA.
DR HSSP; P31872; 1LBO.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; Gp41; 1.
FT NON_TER 1 34
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4196 MW; 0C7CAA60A164B89C CRC64;

Query Match 69.4%; Score 25; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
Db 10 SQIQEKNEQELLELDKWSLWNWF 34

RESULT 12
Q69895_9HIV1
ID Q69895_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69895;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06725; AAA19138.1; -; mRNA.
DR HSSP; P31872; 1LBO.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; Gp41; 1.
FT NON_TER 1 49
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6168 MW; 8077C4815B83281E CRC64;

Query Match 69.4%; Score 25; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
Db 25 SQIQEKNEQELLELDKWSLWNWF 49

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RESULT 13
Q69896 9HIV1
ID Q69896 9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69896;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
EN
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2FS, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06726; AAA19139.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6167 MW; 0277C4815BBD26FE CRC64;

Query Match 69.4%; Score 25; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQQEKNEQELLELDKWSLWNWF 36
Db 25 SQIQQEKNEQELLELDKWSLWNWF 49

RESULT 14
Q9553 9HIV1
ID Q9553 9HIV1 PRELIMINARY; PRT; 118 AA.
AC Q9553;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
EN
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=CAM11;
RX MEDLINE=10957729; PubMed=10957729; DOI=10.1089/08892220050117087;
RA Peter F.N., Bittel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RL AIDS Res. Hum. Retroviruses 16:1319-1324 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=CAM11;
RA Forjongo P.N., Mpoudi E.N., Torimiro J.N., Alemnji G.A., Eno L.T.,
RA Ngngasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the ENBL/GenBank/DBJ databases.
DR EMBL; AF252098; AAG14307.1; -; Genomic DNA.
DR HSSP; P31872; 1LB0.
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DR SMR; Q9553; 1-101.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 14275 MW; 1878D17C292899C0 CRC64;

Query Match 69.4%; Score 25; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 4.5e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQQEKNEQELLELDKWSLWNWF 36
Db 85 SQIQQEKNEQELLELDKWSLWNWF 109

RESULT 15
Q6WH14 9HIV1
ID Q6WH14 9HIV1 PRELIMINARY; PRT; 121 AA.
AC Q6WH14;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
EN
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14715797; DOI=10.1128/JCM.42.1.426-430.2004;
RA Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,
RA Gouvea M.I.F.S., Guimaraes M.A.A.M., De Oliveira F.E.,
RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;
RT "Prevalence of human immunodeficiency virus drug resistance mutations
RT and subtypes in drug-naive, infected individuals in the army health
RT service of Rio de Janeiro, Brazil."
RL J. Clin. Microbiol. 42:426-430 (2004).
DR EMBL; AY285082; AAQ68145.1; -; Genomic RNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 14619 MW; E2791CC4069F12F8 CRC64;

Query Match 69.4%; Score 25; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.6e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQQEKNEQELLELDKWSLWNWF 36
Db 88 SQIQQEKNEQELLELDKWSLWNWF 112

Search completed: March 6, 2006, 16:25:17
Job time : 122 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 16:25:38 ; Search time 28.6667 Seconds
(without alignments)
103.825 Million cell updates/sec

Title: US-09-809-060A-4
Perfect score: 36
Sequence: 1 YTSLLVLLKKSQIQEKNEQELLELDKWSLWNP 36

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
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- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	36	2	US-08-484-223B-240
2	36	100.0	36	2	US-09-082-279B-1360
3	36	100.0	36	2	US-09-315-304B-1360
4	36	100.0	36	2	US-09-834-784-1360
5	36	100.0	36	2	US-09-515-965A-1360
6	36	100.0	36	2	US-09-350-641C-1360
7	36	100.0	36	2	US-09-350-841A-1360
8	25	69.4	36	2	US-09-515-965A-1986
9	25	69.4	36	2	US-09-350-641C-1749
10	25	69.4	36	2	US-09-350-841A-1938
11	25	69.4	138	2	US-09-570-921-10
12	25	69.4	268	2	US-08-965-056-7
13	25	69.4	269	2	US-08-965-056-21
14	24	66.7	36	2	US-09-082-279B-1361
15	24	66.7	36	2	US-09-315-304B-1361
16	24	66.7	36	2	US-09-834-784-1361
17	24	66.7	36	2	US-09-515-965A-1361
18	24	66.7	36	2	US-09-350-641C-1361
19	24	66.7	36	2	US-09-350-841A-1361
20	22	61.1	22	1	US-08-073-028-61
21	22	61.1	22	2	US-08-554-616-61
22	22	61.1	22	2	US-09-515-965A-1674
23	22	61.1	22	2	US-09-350-841A-1704
24	22	61.1	22	2	US-10-005-305-53
25	22	61.1	22	2	US-10-005-305-78
26	22	61.1	23	1	US-08-073-028-62
27	22	61.1	23	2	US-08-484-223B-237

Query Match 100.0%; Score 36; DB 2; Length 36;

ALIGNMENTS

RESULT 1

US-08-484-223B-240

; Sequence 240, Application US/08484223B

; Patent No. 6020459

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

; NUMBER OF SEQUENCES: 245

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,223B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-029

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 240:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; US-08-484-223B-240

Sequence 62, Appl
Sequence 59, Appl
Sequence 421, Appl
Sequence 59, Appl
Sequence 59, Appl
Sequence 1675, Ap
Sequence 59, Appl
Sequence 59, Appl
Sequence 1705, Ap
Sequence 237, Ap
Sequence 54, Appl
Sequence 77, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 789, App
Sequence 790, App
Sequence 789, App

Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 2

US-09-082-279B-1360

; Sequence 1360, Application US/09082279B
; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-1360

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 3

US-09-315-304B-1360

; Sequence 1360, Application US/09315304B

; Patent No. 6348568

; GENERAL INFORMATION:

; APPLICANT: Barney, S.

; APPLICANT: Guthrie, K.

; APPLICANT: Merutka, G.

; APPLICANT: Anwer, M.

; APPLICANT: Lambert, D.

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

; FILE REFERENCE: 7872-052

; CURRENT APPLICATION NUMBER: US/09/315,304B

; PRIOR FILING DATE: 1999-05-20

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1667

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-315-304B-1360

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 4

US-09-834-784-1360

; Sequence 1360, Application US/09834784

; Patent No. 6562787

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/834,784

; PRIOR FILING DATE: 2001-04-13

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-834-784-1360

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 5

US-09-515-965A-1360

; Sequence 1360, Application US/09515965A

; Patent No. 6623741

; GENERAL INFORMATION:

; APPLICANT: Antczak, J.

; APPLICANT: Delmedico, M.

; APPLICANT: Erickson, J.

; APPLICANT: Lambert, D.

; APPLICANT: Sista, P.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-

; FILE REFERENCE: 7872-073

; CURRENT APPLICATION NUMBER: US/09/515,965A

; PRIOR FILING DATE: 2000-02-29

; PRIOR FILING DATE: 1999-05-20

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1994

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-515-965A-1360

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Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36
Db 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36

RESULT 6

US-09-350-641C-1360

; Sequence 1360, Application US/09350641C

; Patent No. 6656906

; GENERAL INFORMATION:

; APPLICANT: Barney, S.

; APPLICANT: Guthrie, K.

; APPLICANT: Merutka, G.

; APPLICANT: Anwer, M.

; APPLICANT: Lambert, D.

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

; FILE REFERENCE: 7872-067

; CURRENT APPLICATION NUMBER: US/09/350.641C

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: 09/315,304

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/082,279

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1757

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-350-641C-1360

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36
Db 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36

RESULT 7

US-09-350-841A-1360

; Sequence 1360, Application US/09350841A

; Patent No. 6750008

; GENERAL INFORMATION:

; APPLICANT: Jeffes, Peter;

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE

; FILE REFERENCE: 7872-066-999

; CURRENT APPLICATION NUMBER: US/09/350.841A

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 1946

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-350-841A-1360

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36
Db 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36

RESULT 8

US-09-515-965A-1986

; Sequence 1986, Application US/09515965A

; Patent No. 6623741

; GENERAL INFORMATION:

; APPLICANT: Antczak, J.

; APPLICANT: Delmedico, M.

; APPLICANT: Erickson, J.

; APPLICANT: Lambert, D.

; APPLICANT: Sista, P.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-

; FILE REFERENCE: 7872-073

; CURRENT APPLICATION NUMBER: US/09/515.965A

; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: 09/315,304

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/082,279

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1994

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1986

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-515-965A-1986

Query Match 69.4%; Score 25; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKQWASLWNWF 36
Db 12 SQIQEKNEQELLELDKQWASLWNWF 36

RESULT 9

US-09-350-641C-1749

; Sequence 1749, Application US/09350641C

; Patent No. 6656906

; GENERAL INFORMATION:

; APPLICANT: Barney, S.

; APPLICANT: Guthrie, K.

; APPLICANT: Merutka, G.

; APPLICANT: Anwer, M.

; APPLICANT: Lambert, D.

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

; FILE REFERENCE: 7872-067

; CURRENT APPLICATION NUMBER: US/09/350.641C

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: 09/315,304

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/082,279

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1757

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1749

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-350-641C-1749

Query Match 69.4%; Score 25; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKQWASLWNWF 36

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Db      12  SGIQEKNEQELLELDKWSLWNWF 36
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RESULT 10
US-09-350-841A-1938
; Sequence 1938, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffes, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350.841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1938
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-841A-1938

Query Match      69.4%; Score 25; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12  SGIQEKNEQELLELDKWSLWNWF 36
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Db      12  SGIQEKNEQELLELDKWSLWNWF 36
|||||

RESULT 11
US-09-570-921-10
; Sequence 10, Application US/09570921
; Patent No. 6455265
; GENERAL INFORMATION:
; APPLICANT: SERRES, PIERRE-FRANCOIS
; TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
; FILE REFERENCE: 106213
; CURRENT APPLICATION NUMBER: US/09/570,921
; CURRENT FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: PCT/FR98/02447
; PRIOR FILING DATE: 1998-11-17
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Human
US-09-570-921-10

Query Match      69.4%; Score 25; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 9.9e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12  SGIQEKNEQELLELDKWSLWNWF 36
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Db      110 SGIQEKNEQELLELDKWSLWNWF 134
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RESULT 12
US-08-965-056-7
; Sequence 7, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
```

```
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: HIV-JRCSP
US-08-965-056-7

Query Match      69.4%; Score 25; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12  SGIQEKNEQELLELDKWSLWNWF 36
|||||
Db      179 SGIQEKNEQELLELDKWSLWNWF 203
|||||

RESULT 13
US-08-965-056-21
; Sequence 21, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-NO. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-21

Query Match 69.4%; Score 25; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQQKNEQELLELDKWASLWNWF 36
Db 180 SQIQQKNEQELLELDKWASLWNWF 204

RESULT 14
US-09-082-279B-1361
; Sequence 1361, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1361
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-082-279B-1361

Query Match 66.7%; Score 24; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQLQEKNEQELL 24
Db 1 YTSLIYSLLEKSQLQEKNEQELL 24

RESULT 15
US-09-315-304B-1361
; Sequence 1361, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
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; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1361
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-315-304B-1361

Query Match 66.7%; Score 24; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YTSLIYSLLEKSQLQEKNEQELL 24

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OM protein - protein search, using sw model

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(without alignments)
154.540 Million cell updates/sec

Title: US-09-809-060A-4
Perfect score: 36
Sequence: 1 YTSLYSLLKESQIQEKNQELLELDKWASLWNWF 36

Scoring table: OIIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	36	100.0	36	3	US-09-809-060-4
2	36	100.0	36	4	US-10-351-641-1360
3	36	100.0	36	4	US-10-663-589-40
4	36	100.0	36	4	US-10-671-282-40
5	36	100.0	36	5	US-10-168-295-5
6	36	100.0	36	5	US-10-168-295-57
7	25	69.4	36	4	US-10-351-641-1749
8	25	69.4	268	3	US-09-854-816-7
9	25	69.4	269	3	US-09-854-816-21
10	24	66.7	36	4	US-10-351-641-1361
11	22	61.1	22	4	US-10-005-305-53
12	22	61.1	22	4	US-10-005-305-78
13	22	61.1	22	5	US-10-950-010-130
14	22	61.1	23	4	US-10-351-641-59
15	22	61.1	23	4	US-10-005-305-54
16	22	61.1	23	4	US-10-005-305-77
17	22	61.1	23	4	US-10-267-682-237
18	22	61.1	23	4	US-10-267-748-237
19	22	61.1	23	5	US-10-168-295-54
20	22	61.1	23	5	US-10-950-010-129
21	22	61.1	24	4	US-10-351-641-789
22	22	61.1	24	4	US-10-351-641-790
23	22	61.1	24	4	US-10-005-305-55
24	22	61.1	24	4	US-10-005-305-76
25	22	61.1	24	4	US-10-005-305-201
26	22	61.1	24	4	US-10-677-807-236
27	22	61.1	24	5	US-10-950-010-128

28 22 61.1 25 4 US-10-893-551-7 Sequence 7, Appli
29 22 61.1 25 4 US-10-005-305-56 Sequence 56, Appl
30 22 61.1 25 4 US-10-005-305-75 Sequence 75, Appl
31 22 61.1 25 5 US-10-950-010-127 Sequence 127, App
32 22 61.1 26 4 US-10-351-641-60 Sequence 60, Appl
33 22 61.1 26 4 US-10-005-305-57 Sequence 57, Appl
34 22 61.1 26 4 US-10-005-305-74 Sequence 74, Appl
35 22 61.1 26 4 US-10-267-682-236 Sequence 236, App
36 22 61.1 26 4 US-10-267-748-236 Sequence 236, App
37 22 61.1 26 5 US-10-168-295-53 Sequence 53, Appl
38 22 61.1 26 5 US-10-950-010-126 Sequence 126, App
39 22 61.1 27 4 US-10-005-305-58 Sequence 58, Appl
40 22 61.1 27 4 US-10-005-305-73 Sequence 73, Appl
41 22 61.1 27 5 US-10-950-010-125 Sequence 125, App
42 22 61.1 28 4 US-10-005-305-59 Sequence 59, Appl
43 22 61.1 28 4 US-10-005-305-72 Sequence 72, Appl
44 22 61.1 28 5 US-10-950-010-124 Sequence 124, App
45 22 61.1 29 4 US-10-351-641-635 Sequence 635, App

ALIGNMENTS

RESULT 1

US-09-809-060-4
; Sequence 4, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild. Carl T.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; TITLE OF INVENTION: Regions of HIV Envelope Proteins
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-4

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYSLLKESQIQEKNQELLELDKWASLWNWF 36
|||||
DB 1 YTSLYSLLKESQIQEKNQELLELDKWASLWNWF 36
|||||

RESULT 2

US-10-351-641-1360
; Sequence 1360, Application US/10351641
; Publication No. US2003018687A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304

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; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1360
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1360

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36

RESULT 3
US-10-663-589-40
; Sequence 40, Application US/10663589
; Publication No. US20040063637A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-40

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36

RESULT 4
US-10-671-282-40
; Sequence 40, Application US/10671282
; Publication No. US20040122214A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
; FILE REFERENCE: TRM-004
; CURRENT APPLICATION NUMBER: US/10/671,282
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/414,439
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: synthesized
US-10-671-282-40

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36

RESULT 5
US-10-168-295-5
; Sequence 5, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Baroudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-5

Query Match      100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36

RESULT 6
US-10-168-295-57
; Sequence 57, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Baroudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-57

Query Match      100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36

RESULT 7
US-10-168-295-57
; Sequence 57, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Baroudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-57

Query Match      100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
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Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
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RESULT 7
US-10-351-641-1749
; Sequence 1749, Application US/10351641
; Publication No. US20030186674A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1749
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1749

Query Match 69.4%; Score 25; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.8e-16; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWASLWNWF 36
Db 12 SQIQEKNEQELLELDKWASLWNWF 36

RESULT 8
US-09-854-816-7
; Sequence 7, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovasnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: HIV-JRC5F
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-854-816-7

Query Match 69.4%; Score 25; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWASLWNWF 36
Db 179 SQIQEKNEQELLELDKWASLWNWF 203

RESULT 9
US-09-854-816-21
; Sequence 21, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovasnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:


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; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-10-950-010-130

Query Match          61.1%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKQASLWNWF 36
Db 1 QOEKNEQELLELDKQASLWNWF 22

RESULT 14
US-10-351-641-59
; Sequence 59, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-59

Query Match          61.1%; Score 22; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKQASLWNWF 36
Db 2 QOEKNEQELLELDKQASLWNWF 23

RESULT 15
US-10-005-305-54
; Sequence 54, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
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; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-54

Query Match          61.1%; Score 22; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKQASLWNWF 36
Db 2 QOEKNEQELLELDKQASLWNWF 23

Search completed: March 6, 2006, 16:32:48
Job time : 97.3333 secs
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GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:28:08 ; Search time 10.3333 Seconds
 (without alignments)
 69.679 Million cell updates/sec

Title: US-09-809-060A-4

Perfect score: 36

Sequence: 1 YTSIIYSLLEKSIQOEKNEQELLELDKWSLWNWF 36

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OLIGO Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications AA.New.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	61.1	35	6	US-10-506-796A-1
2	22	61.1	36	6	US-10-841-956A-1
3	22	61.1	36	6	US-10-506-796A-3
4	22	61.1	36	7	US-11-029-003-1
5	22	61.1	36	7	US-11-187-687-22
6	22	61.1	37	7	US-11-112-277-33
7	22	61.1	44	7	US-11-089-426-10
8	22	61.1	44	7	US-11-187-687-24
9	22	61.1	145	7	US-11-084-858-11
10	22	61.1	171	6	US-10-506-796A-9
11	22	61.1	267	6	US-10-841-956A-4
12	22	61.1	269	6	US-10-841-956A-8
13	22	61.1	270	6	US-10-841-956A-5
14	22	61.1	281	6	US-10-841-956A-7
15	22	61.1	282	6	US-10-841-956A-6
16	22	61.1	293	6	US-10-841-956A-9
17	22	61.1	354	7	US-11-053-100-27
18	22	61.1	356	7	US-11-053-100-36
19	22	61.1	357	7	US-11-053-100-30
20	22	61.1	357	7	US-11-053-100-33
21	22	61.1	504	7	US-11-053-100-28
22	22	61.1	506	7	US-11-053-100-37
23	22	61.1	507	7	US-11-053-100-31
24	22	61.1	507	7	US-11-053-100-34
25	22	61.1	654	7	US-11-053-100-29

26	22	61.1	656	7	US-11-053-100-38	Sequence 38, Appl
27	22	61.1	657	7	US-11-053-100-32	Sequence 32, Appl
28	22	61.1	657	7	US-11-053-100-35	Sequence 35, Appl
29	22	61.1	856	6	US-10-510-947-8	Sequence 8, Appl
30	22	61.1	856	7	US-11-042-988-13	Sequence 13, Appl
31	22	61.1	856	7	US-11-135-235-1	Sequence 1, Appl
32	16	44.4	36	6	US-10-506-796A-5	Sequence 5, Appl
33	15	41.7	15	7	US-11-045-024-13381	Sequence 13381, A
34	15	41.7	601	7	US-11-014-842A-37	Sequence 37, Appl
35	15	41.7	613	7	US-11-014-842A-33	Sequence 33, Appl
36	15	41.7	669	7	US-11-014-842A-29	Sequence 29, Appl
37	15	41.7	681	7	US-11-014-842A-25	Sequence 25, Appl
38	15	41.7	789	7	US-11-014-842A-39	Sequence 39, Appl
39	15	41.7	801	7	US-11-014-842A-35	Sequence 35, Appl
40	15	41.7	857	7	US-11-014-842A-31	Sequence 31, Appl
41	15	41.7	869	7	US-11-014-842A-27	Sequence 27, Appl
42	14	38.9	36	6	US-10-506-796A-7	Sequence 7, Appl
43	11	30.6	11	7	US-11-045-024-101	Sequence 101, App
44	11	30.6	11	7	US-11-045-024-103	Sequence 103, App
45	11	30.6	11	7	US-11-045-024-983	Sequence 983, App

ALIGNMENTS

RESULT 1
 US-10-506-796A-1
 ; Sequence 1, Application US/10506796A
 ; Publication No. US200600113831A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MOR, Tsafir
 ; APPLICANT: MATOBA, Nobuyuki
 ; APPLICANT: ARNTZEN, Charles
 ; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
 ; FILE REFERENCE: 01231.0006U2
 ; CURRENT APPLICATION NUMBER: US/10/506,796A
 ; PRIOR FILING DATE: 2004-09-03
 ; PRIOR APPLICATION NUMBER: PCT/US03/07073
 ; PRIOR FILING DATE: 2003-03-06
 ; PRIOR APPLICATION NUMBER: 60/362,247
 ; PRIOR FILING DATE: 2002-03-06
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 1
 ; TYPE: PRT
 ; LENGTH: 35
 ; ORGANISM: Human immunodeficiency virus type 1
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(35)
 ; OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
 US-10-506-796A-1

Query Match 61.1%; Score 22; DB 6; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.7e-15;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKWSLWNWF 36
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 Db 4 QOEKNEQELLELDKWSLWNWF 25

RESULT 2
 US-10-841-956A-1
 ; Sequence 1, Application US/10841956A
 ; Publication No. US20050281829A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TAN HEHIR, CRISTINA A.
 ; APPLICANT: MEZO, ADAM R.
 ; APPLICANT: PETERS, ROBERT T.
 ; APPLICANT: STATTEL, JAMES M.
 ; APPLICANT: PALOMBELLA, VITO J.
 ; APPLICANT: BITONTI, ALAN R.

; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-1

Query Match 61.1%; Score 22; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-15; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 QOEKNEQELLELDKWASLWNWF 36
DB 15 QOEKNEQELLELDKWASLWNWF 36

RESULT 3
US-10-506-796A-3
; Sequence 3, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-506-796A-3

Query Match 61.1%; Score 22; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-15; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 QOEKNEQELLELDKWASLWNWF 36
DB 5 QOEKNEQELLELDKWASLWNWF 26

RESULT 4
US-11-029-003-1
; Sequence 1, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEL, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029,003
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539,207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487,964

; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469,600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-029-003-1

Query Match 61.1%; Score 22; DB 7; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-15; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 QOEKNEQELLELDKWASLWNWF 36
DB 15 QOEKNEQELLELDKWASLWNWF 36

RESULT 5
US-11-187-687-22
; Sequence 22, Application US/11187687
; Publication No. US20060019347A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Ho Sung
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Hays, Anna-Maria
; APPLICANT: Wilson, Troy E.
; APPLICANT: Litzinger, David C.
; APPLICANT: Mariani, Roberto
; APPLICANT: Kimmel, Bruce E.
; APPLICANT: Keefe, William M.
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
; FILE REFERENCE: AMBX-0041.000US
; CURRENT APPLICATION NUMBER: US/11/187,687
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: 60/590,035
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: 60/659,709
; PRIOR FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-22

Query Match 61.1%; Score 22; DB 7; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-15; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 QOEKNEQELLELDKWASLWNWF 36
DB 15 QOEKNEQELLELDKWASLWNWF 36

RESULT 6
US-11-112-277-33
; Sequence 33, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228

; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T20 Analogue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 37
; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-33

Query Match 61.1%; Score 22; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 15 QOEKNEQELLELDKWASLWNWF 36

RESULT 7

US-11-089-426-10
; Sequence 10, Application US/11089426
; Publication No. US20050261229A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Wesolowski, John
; TITLE OF INVENTION: FC Fusion Proteins For Enhancing the Immunogenicity of
; TITLE OF INVENTION: Protein and Peptide Antigens
; FILE REFERENCE: LEX-007
; CURRENT APPLICATION NUMBER: US/11/089,426
; CURRENT FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2000-07-21
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/144,965
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fused
; OTHER INFORMATION: polypeptide from pDC-muFC vector
US-11-089-426-10

Query Match 61.1%; Score 22; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 13 QOEKNEQELLELDKWASLWNWF 34

RESULT 8

US-11-187-687-24
; Sequence 24, Application US/11187687
; Publication No. US20060019347A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Ho Sung.
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Hays, Anna-Maria
; APPLICANT: Wilson, Troy E.
; APPLICANT: Litzinger, David C.
; APPLICANT: Mariani, Roberto
; APPLICANT: Kimmel, Bruce E.

; APPLICANT: Keefe, William M.
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
; FILE REFERENCE: AMBX-0041.00US
; CURRENT APPLICATION NUMBER: US/11/187,687
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: 60/590,035
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: 60/659,709
; PRIOR FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-24

Query Match 61.1%; Score 22; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 23 QOEKNEQELLELDKWASLWNWF 44

RESULT 9

US-11-084-858-11
; Sequence 11, Application US/11084858
; Publication No. US2005021678A1
; GENERAL INFORMATION:
; APPLICANT: BRUST, Stefan
; APPLICANT: KNAPP, Stefan
; APPLICANT: GERKEN, Manfred
; APPLICANT: GUERTLER, Lutz
; TITLE OF INVENTION: Peptides derived from a retrovirus of
; TITLE OF INVENTION: the HIV group, and their use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/084,858
; FILING DATE: 21-Mar-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/000,321
; FILING DATE: 04-Dec-2001
; APPLICATION NUMBER: 09/131,551
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 58315/106/BEAK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>

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;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-084-858-11

Query Match      61.1%; Score 22; DB 7; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKWASLWNWF 36
Db 120 QQEKNEQELLELDKWASLWNWF 141

RESULT 10
US-10-506-796A-9
; Sequence 9, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Teafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note = synthetic construct
US-10-506-796A-9

Query Match      61.1%; Score 22; DB 6; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKWASLWNWF 36
Db 133 QQEKNEQELLELDKWASLWNWF 154

RESULT 11
US-10-841-956A-4
; Sequence 4, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence; Synthetic
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; OTHER INFORMATION: construct
US-10-841-956A-4

Query Match      61.1%; Score 22; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKWASLWNWF 36
Db 246 QQEKNEQELLELDKWASLWNWF 267

RESULT 12
US-10-841-956A-8
; Sequence 8, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence; Synthetic
US-10-841-956A-8

Query Match      61.1%; Score 22; DB 6; Length 269;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKWASLWNWF 36
Db 248 QQEKNEQELLELDKWASLWNWF 269

RESULT 13
US-10-841-956A-5
; Sequence 5, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence; Synthetic
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-841-956A-5

Query Match 61.1%; Score 22; DB 6; Length 270;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 QQEKNEQELLELDKWSLWVNF 36
Db 15 QQEKNEQELLELDKWSLWVNF 36

RESULT 14

US-10-841-956A-7
; Sequence 7, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-841-956A-7

Query Match 61.1%; Score 22; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 QQEKNEQELLELDKWSLWVNF 36
Db 15 QQEKNEQELLELDKWSLWVNF 36

RESULT 15

US-10-841-956A-6
; Sequence 6, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-841-956A-6

Query Match 61.1%; Score 22; DB 6; Length 282;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 QQEKNEQELLELDKWSLWVNF 36
Db 261 QQEKNEQELLELDKWSLWVNF 282

Search completed: March 6, 2006, 16:33:26
Job time : 11.3333 secs

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